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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 01:03:53 ; Search time 323.574 Seconds  
 (without alignments)  
 4675.326 Million cell updates/sec

Title: US-10-734-373-59  
 Perfect score: 690  
 Sequence: 1 atggattccacactgtgtc.....gaacaattgagccagaagtt 690

Scoring table: IDENTITY NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications NA New:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US08 NEW PUB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/US06 NEW PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US07 NEW PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/PCT NEW PUB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US09 NEW PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10 NEW PUB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US11 NEW PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US12 NEW PUB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US13 NEW PUB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US14 NEW PUB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US15 NEW PUB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US16 NEW PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60 NEW PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38.8	5.6	528	US-09-925-065A-597659	Sequence 597659,
2	35.8	5.2	2427	US-09-925-065A-704634	Sequence 704634,
3	35.6	5.2	8196	US-10-678-790-53	Sequence 53, Appl
4	35.4	5.1	576	US-09-925-065A-408802	Sequence 408802,
5	35.4	5.1	1576	US-09-925-065A-408803	Sequence 408803,
6	35.2	5.1	1576	US-10-973-115B-301	Sequence 301, App
7	35.2	5.1	2263	US-10-131-826A-301	Sequence 87, Appl
8	35.2	5.1	2263	US-11-245-147-87	Sequence 768990,
9	34	4.9	615	US-09-925-065A-768990	Sequence 316303,
10	33.8	4.9	522	US-09-925-065A-316303	Sequence 621004,
11	33.8	4.9	598	US-09-925-065A-621004	Sequence 32454,
12	33.6	4.9	576	US-09-925-065A-32454	Sequence 329025,
13	33.2	4.8	583	US-09-925-065A-329025	Sequence 470072,
14	33.2	4.8	607	US-09-925-065A-470072	Sequence 782109,
15	33.2	4.8	629	US-09-925-065A-782109	Sequence 843006,
16	33.2	4.8	629	US-09-925-065A-843006	Sequence 794377,
17	33.2	4.8	630	US-09-925-065A-794377	Sequence 850295,
18	33.2	4.8	630	US-09-925-065A-850295	Sequence 288846,
19	33.2	4.8	978	US-09-925-065A-288846	Sequence 47484, A
20	33.2	4.8	1357	US-10-750-185-47484	

21	33.2	4.8	1357	8	US-10-750-623-47484	Sequence 47484, A
22	33	4.8	468	6	US-09-925-065A-223423	Sequence 223423,
23	33	4.8	468	6	US-09-925-065A-223424	Sequence 223424,
24	33	4.8	563	6	US-09-925-065A-300378	Sequence 300378,
25	33	4.8	563	6	US-09-925-065A-300379	Sequence 300379,
26	33	4.8	600	6	US-09-925-065A-523519	Sequence 523519,
27	33	4.8	935	6	US-09-925-065A-523519	Sequence 523519,
28	33	4.8	1119	6	US-09-925-065A-282212	Sequence 282212,
29	33	4.8	1597	8	US-10-750-623-33998	Sequence 33998, A
30	33	4.8	1597	8	US-10-750-623-33998	Sequence 33998, A
31	32.8	4.8	602	6	US-09-925-065A-879502	Sequence 879502,
32	32.8	4.8	604	6	US-09-925-065A-627547	Sequence 627547,
33	32.8	4.8	1185	6	US-09-925-065A-24597	Sequence 24597, A
34	32.8	4.8	1185	6	US-09-925-065A-24597	Sequence 24597, A
35	32.4	4.7	604	6	US-09-925-065A-627546	Sequence 627546,
36	32.4	4.7	3406	6	US-09-925-065A-682775	Sequence 682775,
37	32	4.6	434	6	US-09-925-065A-224372	Sequence 224372,
38	32	4.6	434	6	US-09-925-065A-224373	Sequence 224373,
39	32	4.6	539	6	US-09-925-065A-192076	Sequence 192076,
40	32	4.6	612	6	US-09-925-065A-735792	Sequence 735792,
41	32	4.6	612	6	US-09-925-065A-735793	Sequence 735793,
42	32	4.6	653	6	US-09-925-065A-785430	Sequence 785430,
43	32	4.6	653	6	US-09-925-065A-799107	Sequence 799107,
44	31.8	4.6	417	6	US-09-925-065A-171032	Sequence 171032,
45	31.8	4.6	548	6	US-09-925-065A-282213	Sequence 282213,

## ALIGNMENTS

## RESULT 1

US-09-925-065A-597659  
 ; Sequence 597659, Application US/09925065A  
 ; Publication No. US20040181048A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single  
 ; Nucleotide Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 10827.135  
 ; CURRENT APPLICATION NUMBER: US/09/925,065A  
 ; PRIOR FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: US 60/243,096  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 60/252,147  
 ; PRIOR FILING DATE: 2000-11-20  
 ; PRIOR APPLICATION NUMBER: US 60/250,092  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/261,766  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/289,846  
 ; PRIOR FILING DATE: 2001-05-09  
 ; NUMBER OF SEQ ID NOS: 957086  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 597659  
 ; LENGTH: 528  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-925-065A-597659

Query Match 5.6%; Score 38.8; DB 6; Length 528;

Best Local Similarity 49.0%; Pred. No. 0.17;

Matches 103; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY	10	AACACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCGCGAAACGATTTCGA	69
DB	255	ACCACGTAGTCAACTATATTTCCAAACAAATCTCGAGAAATAGCTCCAGATACACA	314
QY	70	GACCAAGACTGGGTGATGCCCATTCCTTTCGCGGCTCCGCGAGCAGAGTCCCTA	129
DB	315	GATTAAGAATGGGGCTCCCAACCAACACCTTCCCTACCAACAGCTCTGCTC	374
QY	130	AAAGGAAGGTAGTACTCTTGTGTCATCGAAGACGCACTGTGTCAGAAAGCAG	189

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Db 375 AAATACCACACAACTGATTTTAACTAAGGAAAGATCAAGCAGATGAACCTA 434

Qy 190 ATAGTGGAGCAGATTCTTGAAGAGGAATCA 219  
Db 435 TGAATTGAAGCTATTATTGTAATGAATGA 464

RESULT 2

US-09-925-065A-704634  
; Sequence 704634, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 704634  
; LENGTH: 2427  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-704634

Query Match 5.2%; Score 35.8; DB 6; Length 2427;  
Best Local Similarity 52.3%; Pred. No. 2.8;  
Matches 79; Conservative 0; Mismatches 72; Indels 0; Gaps 0;  
Qy 512 ATGAGGATGTCAAAATGCAATTCGGGTCTCTATCGAGGACTTAATGATGATATA 571  
Db 35 AAGTGAATATACAAAGCCAGAGTCACTTCATAGAGGAGATCAATTCGATTTGAATA 94  
Qy 572 CGGTTAGAACTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGGA 631  
Db 95 TGGAAAGAGATTTGATATTTTAAAGGCTCTTATGGGAAAGGAAAGAAATAAAGAAAA 154  
Qy 632 GACCTTCATTCCTCCAAAGCAGAAACGAA 662  
Db 155 CATCATATTTCTCACTGTAGCAGAAAAACAA 185

RESULT 3  
US-10-678-790-53/c  
; Sequence 53, Application US/10678790  
; Publication No. US20050287530A1  
; GENERAL INFORMATION:  
; APPLICANT: Croce, Carlo  
; TITLE OF INVENTION: TCL-1b Gene and Protein and Related Methods and  
; FILE REFERENCE: CRO01.NP003  
; CURRENT APPLICATION NUMBER: US/10/678,790  
; CURRENT FILING DATE: 2003-10-02  
; PRIOR FILING DATE: 2003-10-02  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR FILING DATE: 1999-03-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 53  
; LENGTH: 8196  
; TYPE: DNA

; ORGANISM: mouse  
US-10-678-790-53

Query Match 5.2%; Score 35.6; DB 8; Length 8196;  
Best Local Similarity 48.1%; Pred. No. 5.8; 109; Indels 0; Gaps 0;  
Matches 101; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
Qy 106 CTTCCGCGAGACCAGAAAGTCCCTTAAAGGAAGAGGTAGACTCTTGGTCTGGACATCGAA 165  
Db 4213 CATGCCAAGAGAGAGATAAAGGAGAAAGAGAGAGAAATAAAGGCTAGAGACTAAGAA 4154  
Qy 166 ACAGCCACTCGTGCAGGAAAGAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAG 225  
Db 4153 AGCTTAAAGAGAGAGAGGCTAAGAGATAGAGATTAAGAGATTAAGAGGAGAGAGT 4094  
Qy 226 GCACCTTAAATGACCATTCCTCTGTTCTGCTTCAAGCTTAACTACTGACATGACTCTT 285  
Db 4093 GAGGTGGGCCCAACAGCCCCCTTGTATCTGTTGTTAGGTAACTGGGAGAGTCTA 4034  
Qy 286 GATGAGATGTCAAGAGACTGGTTCATGCTC 315  
Db 4033 GCCTAAAGGGCAGAAAGCTTGGGGCATTGTC 4004

RESULT 4

US-09-925-065A-408802  
; Sequence 408802, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 408802  
; LENGTH: 576  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-408802

Query Match 5.1%; Score 35.4; DB 6; Length 576;  
Best Local Similarity 61.3%; Pred. No. 1.9;  
Matches 57; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
Qy 464 CAGTGTGGCGAAATTTCCACCATTCCTCTCTCCAGGACATATTAATGAGATCTCA 523  
Db 425 CAGGCTTTGCAAGCTTACCTCTCTCTCCAGGACTCAGATGAAAGAAAA 484  
Qy 524 AAANTGCAATTTGGGTCTCTCATCGGAGACTTA 556  
Db 485 TAAATGCAAGGTAAGCTTCACTCGGTCTCTCA 517

RESULT 5

US-09-925-065A-408803  
; Sequence 408803, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single



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; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 301
; LENGTH: 1576
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-301

Query Match
Best Local Similarity 5.1%; Score 35.2; DB 8; Length 1576;
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 344 TATGTATAGATGACGAGGCAATCATGATAAGACATCATCTTAAAGCAACTTTA 403
DB 1032 TTGTGCGAAGTATTTTCGGGTATAGAGAAATTTGAATTTTCTTAAGACATACAT 973

QY 404 GTGTGATTTTGAAGGCTGGAGACACTAATACTACTTAGAGCTTCCCGAGAGGAG 463
DB 972 AAGTGAAGAAGGCAAAACAGGAGGCATTGATTTCTAATCTGTACTCGAGGTTGAGCTG 913

QY 464 CAGTCGTTGGCAATTTCCACCTTCTCTTCCAGACATATAATAGGATGTCA 523
DB 912 CATTAGTTTTCATTTGGCAAGATTTTGTCTTTTAGCAGAGAATCATGAAGATAATT 853

QY 524 AAAA 527
DB 852 ATAA 849

RESULT 8
US-11-245-147-87/C
; Sequence 87, Application US/11245147
; Publication No. US20060030541A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHABER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RANADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/11/245,147
; CURRENT FILING DATE: 2005-10-07
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 87
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-245-147-87

Query Match
Best Local Similarity 5.1%; Score 35.2; DB 9; Length 2263;
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 344 TATGTATAGATGACGAGGCAATCATGATAAGACATCATCTTAAAGCAACTTTA 403
DB 865 TTGTGCGAAGTATTTTCGGGTATAGAGAAATTTGAATTTTCTTAAGACATACAT 806

QY 404 GTGTGATTTTGAAGGCTGGAGACACTAATACTACTTAGAGCTTCCCGAGAGGAG 463
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DB 805 AAGTGAAGAAGGCAAAACAGGAGGCATTGATTTCTAATCTGTACTTCGAGAGTTGAGCTG 746
QY 464 CAGTCGTTGGCAAAATTTCCACCTTCTCTTCCAGACATATAATAGGATGTCA 523
DB 745 CATTAGTTTTCATTTGGCAAGATTTTGTCTTTTAGCAGAGAATCATGAAGATAATT 686

QY 524 AAAA 527
DB 685 ATAA 682

RESULT 9
US-09-925-065A-768990/C
; Sequence 768990, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 768990
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-768990

Query Match
Best Local Similarity 4.9%; Score 34; DB 6; Length 615;
Matches 55; Conservative 1; Mismatches 36; Indels 0; Gaps 0;

QY 175 CQTGCGAAGCAGATATGAGCAGATTTCTGGAAGAGGAATCAGATGAGGCACTTAA 234
DB 429 CTCGAGATATCAGCCAGATGTGAAGTTTATCCAGGTACTTTAGAGAGGAGAACTTAA 370

QY 235 ATGACCATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 266
DB 369 ATCAGAAATGCTATGTTCAITTTTCYCTTA 338

RESULT 10
US-09-925-065A-316303
; Sequence 316303, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
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; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 316303
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-316303

Query Match      4.9%; Score 33.8; DB 6; Length 522;
Best Local Similarity 49.7%; Pred. No. 5.6;
Matches 83; Conservative 1; Mismatches 83; Indels 0; Gaps 0;

QY 350 TAAGAATGGACCAAGCAATCATGGATAGACATCATCTTAAAGCAACTTTAGTGTGA 409
    |||||
Db 211 TAATATCTGAAAGTAGTGTGAGGTTAAAGACATACATGATGAATTTGAATTTGA 270
    |||||
QY 410 TTTTCGAAGCTGGAGACACTAATACTACTTAGAGCCTTACCCAGAGAGCGAGTCG 469
    |||||
Db 271 TTTTGAAGTCTGTCAATATCAAAAGTTAAACACTTCTCGAATGATGATCAAG 330
    |||||
QY 470 TTGGCGAAATTCACCATTCCTCTCTCCAGGACATCTAATGAG 516
    |||||
Db 331 TCATGTGAAATATATAGTCATTTATTAGCCAAAGGCATATTGATCRG 377
    |||||

RESULT 11
US-09-925-065A-621004
; Sequence 621004, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 621004
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-621004

Query Match      4.9%; Score 33.8; DB 6; Length 598;
Best Local Similarity 50.3%; Pred. No. 5.9;
Matches 83; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 46 TGGCATGTCCGAAACGATTTGACAGACCAAGAACTGGGTGATGCCCATTCCTTGACCG 105
    |||||
Db 42 TGAATGAATCAGAGAGGAGGACATCCAGATAGGCGGCTTGTGATGGAAGG 101
    |||||
QY 106 CTTCCGAGACAGAGTCCCTAAAGGAGAGGTAGCACTCTGTGCTGGACATCGAA 165
    |||||
Db 102 CTTTGGGAGACCAATYGGAAATTTGACAGAGAGAACTGCTATGCTGAATGTAA 161
    |||||
QY 166 ACAGGCACTGTCCAGAAAGCAGATAGTGGAGCAGATCTTGAAA 210
    |||||
Db 162 ACAGTTACTGTGCTGTGTGGAAATAGACTGGATGGGCAA 206
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RESULT 12
US-09-925-065A-332454/c
; Sequence 332454, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 332454
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-332454

Query Match      4.9%; Score 33.6; DB 6; Length 576;
Best Local Similarity 55.3%; Pred. No. 6.7;
Matches 63; Conservative 1; Mismatches 50; Indels 0; Gaps 0;

QY 338 GCTCCCTATGTATGAAGATCGACGCGCAATCATGGATAAGAACATCATCTTAAGCAA 397
    |||||
Db 335 GTTCTGTATTTAAAGTAATCCAGGAATGATTAAGGCTAGCTATTATTATTCA 276
    |||||
QY 398 ACTTTAGTGTGATTTTCGAAGCTGGAGACACTAATACTACTAGAGCCTTCA 451
    |||||
Db 275 AATTTTCAGTGTCTTTTGAAGAAATGATCATGCTACTTTCTATTATTGTTTA 222
    |||||

RESULT 13
US-09-925-065A-329025
; Sequence 329025, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 329025
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-329025

Query Match      4.8%; Score 33.2; DB 6; Length 583;
Best Local Similarity 48.4%; Pred. No. 8.9;
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Matches 92; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 498 TCAGGACATACATAGGATGTCACAAATGCAATTTGGGGTCTCTCATCGGAGACTTAA 557  
Db 315 TCTAGAGCCACATACACAGAAATATAATATGCAATTCATAAAGAAAAATGAACCTTA 374  
QY 558 ATGGAGTAATACGGTTAGAACTCTCTGAACTCTACAGATTTCGGTGGAGAGCAG 617  
Db 375 AIGTACCTAAATATATATGCAATATGTAATCTCCAAATAAGTGGGAGAAAAATG 434  
QY 618 TCATCAGATGGGAGCCTTCATCTCCCAAGCAGAAACGAAAAATGGAGAGACAAT 677  
Db 435 TGATGACAGATCTCAAAATCTGTTTCAGAAATCAATGACTCAATAGCAAGAAAAAA 494  
QY 678 TGAGCCAGAA 687  
Db 495 ACAGTAAGAA 504

RESULT 14  
US-09-925-065A-470072/c  
; Sequence 470072, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 470072  
; LENGTH: 607  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-470072

Query Match 4.8%; Score 33.2; DB 6; Length 607;  
Best Local Similarity 51.3%; Pred. No. 9.1;  
Matches 77; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 477 AATTTCCACCATTCCTCTTCCAGACATCTAATGAGGATCTCAAAAATGCAATTGG 536  
Db 528 AATAGTAGCATCTCTTGGCTCTCTAGGACTAAAGTAAGATATATAATAGCCTTTA 469  
QY 537 GGTCTCTATCGGAGGACTTAAATGATGTAATACGGTTAGAACTCTCTGAACTCTACA 596  
Db 468 TGGCAGAAATCTTAGGCTTAAGAGAAATGAAGCAGAAAAACCTGCTTAGCTCTTAAG 409  
QY 597 GAGATTGCTTGGAGAGGAGCTCATGAGAA 626  
Db 408 AAGTCCTTTACAGAAAAACATATGATGGA 379

RESULT 15  
US-09-925-065A-782109/c  
; Sequence 782109, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 782109  
LENGTH: 629  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-782109

Query Match 4.8%; Score 33.2; DB 6; Length 629;  
Best Local Similarity 49.4%; Pred. No. 9.3;  
Matches 86; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 357 GGACCCAGCAATCATGGATAAGAACATCATCTTAAAGCAAACTTTAGTGTGATTTGGA 416  
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QY 417 AAGGCTGGAGACACTAATCTACTTAGAGCCTTCCAGGAGAGGAGCAGTCGTTGGCGA 476  
Db 423 TACCATGATAATGTTAATAGTACTAATGATTTAACAATAATTTAAGGTAGTTGGGA 364  
QY 477 AATTTCCACCATTCCTCTTCCAGACATCTAATGAGGATCTCAAAAATGTC 530  
Db 363 AGTAAGAGAGTACAAAATCTCAAGGATAAAAAGGAATAAATAGATATATGC 310

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Job time : 324.574 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 00:04:28 ; Search time 4572.81 Seconds  
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Title: US-10-734-373-57

Perfect score: 888  
Sequence: 1 agcaaaagcgggtgacaaa.....aaaaaacaccccttctcta 888

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*  
2: gb\_in.\*  
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4: gb\_cm.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
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8: gb\_pi.\*  
9: gb\_pi.\*  
10: gb\_sts.\*  
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12: gb\_un.\*  
13: gb\_vi.\*  
14: gb\_htg.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	888	100.0	888	6	AR254669 Sequence
2	888	100.0	888	6	AR455544 Sequence
3	888	100.0	888	6	AX225029 Sequence
4	886.4	99.8	891	6	AR254664 Sequence
5	886.4	99.8	891	6	AR455539 Sequence
6	886.4	99.8	891	6	AX225022 Sequence
7	884.4	99.6	888	6	AR254666 Sequence
8	884.4	99.6	888	6	AR455541 Sequence
9	884.4	99.6	888	6	AX225025 Sequence
10	880	99.1	890	13	FLANSEQUTE
11	870.4	98.0	890	13	FLANSEQEN
12	868.8	97.8	890	13	FLANSEQON
13	868.8	97.8	890	13	FLANSEQNM
14	867.2	97.7	890	13	FLANSEQNY
15	865.6	97.5	890	13	AY855345
16	865.6	97.5	890	13	FLANSEQOR
17	865.6	97.5	890	13	FLANSEQAN
18	857.6	96.6	890	13	FLANSEQFON

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20	834.8	94.0	838	13	AF001667	AF001667 Influenza
21	834.8	94.0	838	13	AF001668	AF001668 Influenza
22	834.8	94.0	838	13	AF001671	AF001671 Influenza
23	834.8	94.0	838	13	AF001673	AF001673 Influenza
24	831.5	93.6	838	13	AF001669	AF001669 Influenza
25	828.4	93.3	838	13	AF001664	AF001664 Influenza
26	825.2	92.9	838	13	AF001662	AF001662 Influenza
27	825.2	92.9	838	13	AF001670	AF001670 Influenza
28	810.8	91.3	838	13	AF001663	AF001663 Influenza
29	810.8	91.3	838	13	AF001672	AF001672 Influenza
30	807.6	90.9	838	13	AF001665	AF001665 Influenza
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32	793.6	89.4	890	13	FLANSWALNY	FLANSWALNY Influenza A
33	788.8	88.8	890	13	IAU9486	IAU9486 Influenza A
34	788.8	88.8	890	13	FLANSRTNJ	FLANSRTNJ Influenza A
35	788.4	88.8	886	13	AY633120	AY633120 Influenza
36	785.6	88.5	890	13	AY650274	AY650274 Influenza
37	784	88.3	890	13	AY611528	AY611528 Influenza
38	784	88.3	890	13	AY646082	AY646082 Influenza
39	784	88.3	890	13	AY648291	AY648291 Influenza
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41	780.8	87.9	897	13	AY633328	AY633328 Influenza A
42	780.2	87.9	865	13	IAU85376	IAU85376 Influenza A
43	777.6	87.6	890	13	AF285889	AF285889 Influenza A
44	777.6	87.6	890	13	FLANSWCHI	FLANSWCHI Influenza A
45	777.6	87.6	890	13	INA410597	INA410597 Influenza

#### ALIGNMENTS

RESULT 1  
AR254669 888 bp DNA linear PAT 20-DEC-2002  
LOCUS Sequence 57 from patent US 6482414.  
DEFINITION AR254669  
ACCESSION AR254669  
VERSION AR254669.1 GI:27303690  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 888)

AUTHORS Dowling,P.W. and Youngner,J.S.

TITLE Cold-adapted equine influenza viruses

JOURNAL Patent: US 6482414-A 57 19-NOV-2002;

The University of Pittsburgh-of the Commonwealth System of Higher

Education; Pittsburgh, PA

FEATURES Location/Qualifiers

source 1..888

/organism="unknown"

/mol\_type="genomic DNA"

#### ORIGIN

Query Match	100.0%;	Score 888;	DB 6;	Length 888;
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Matches 888;	Conservative 0;	Gaps 0;		
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Db	61	ACTGTCTTCTTGGCAGTCGCGAACAGATTGGAGACCAAGACTGGGTGATGCCCAT	120	
Qy	121	TCCTTACCGGCTTCGCGAGACACAGAAGTCCTTAAAGAGAGAGTAGCCTTTGGTC	180	
Db	121	TCCTTACCGGCTTCGCGAGACACAGAAGTCCTTAAAGAGAGAGTAGCCTTTGGTC	180	
Qy	181	TGGACATCGAAACACCACTCGTGCAGGAAGACAGATAGTGAGAGAGG	240	
Db	181	TGGACATCGAAACACCACTCGTGCAGGAAGACAGATAGTGAGAGAGG	240	



TITLE Cold-adapted equine influenza viruses  
JOURNAL Patent: WO 0160849-A 39 23-AUG-2001;  
(US) UNIV. OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION

## FEATURES

Location/Qualifiers

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/organism="Equine influenza virus H3N8"

/mol\_type="unassigned DNA"

/db\_xref="taxon:31660"

27..719

/note="unnamed protein product"

/codon\_start=1

/protein\_id="CAC69596.1"

/db\_xref="GI:15555103"

GRGSTGLDIETATRAKQIVQILLESDEALMTIASPASYLITDMTIDMSRDW  
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SPLPLPGHTNEDVKNAGVILGGLKWNIDNTRVISETLQRFARSSHENGRPSFPKQ  
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## CDS

## ORIGIN

Query Match 100.0%; Score 888; DB 6; Length 888;  
Best Local Similarity 100.0%; Pred. No. 2.8e-209; Indels 0; Gaps 0;  
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGCTGACAAAACATATGATTCACACCTGTGTCAAGCTTTCAAGTAG 60  
DB 1 AGCAAAAGCAGGCTGACAAAACATATGATTCACACCTGTGTCAAGCTTTCAAGTAG 60

QY 61 ACTGTTTCTTTGGCATGTCGCAAAACGATTTGCAGACCAAGAACTGGTGATGCCCAT 120  
DB 61 ACTGTTTCTTTGGCATGTCGCAAAACGATTTGCAGACCAAGAACTGGTGATGCCCAT 120

QY 121 TCCTTGACCGGCTTCGCGAGACGAGAGTCCCTTAAAGGAAGAGGTAGCACTCTTGTC 180  
DB 121 TCCTTGACCGGCTTCGCGAGACGAGAGTCCCTTAAAGGAAGAGGTAGCACTCTTGTC 180

QY 181 TGCACATCGAAGCAGCACTCTGTCAGGAAGCAGATAGTGAGCAGATCTTGGAGAGG 240  
DB 181 TGCACATCGAAGCAGCACTCTGTCAGGAAGCAGATAGTGAGCAGATCTTGGAGAGG 240

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DB 241 AATCAGATGAGCCTTAAATGACCACTTGCCTCTGCTTCTGCTTCAAGCTTTAACTG 300

QY 301 ACATGACTCTTGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCAAGCAAGAAAGTAA 360  
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QY 361 CAGGCTCCCTATGATAGATGAGCAGGCAATCATGATAGAAACATCATCTTTAAAG 420  
DB 361 CAGGCTCCCTATGATAGATGAGCAGGCAATCATGATAGAAACATCATCTTTAAAG 420

QY 421 CAACCTTTAGTGTGATTTTCGAAGGCTCGAGACACTAACTACTTACCTAGAGCTTCACCG 480  
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QY 481 AAGAGGAGCAGTCTGTTGGGAAATTCACCATGCTTCTTCTTCCAGGACATCTAAATG 540  
DB 481 AAGAGGAGCAGTCTGTTGGGAAATTCACCATGCTTCTTCTTCCAGGACATCTAAATG 540

QY 541 AGGATGTCAAAAATGCAATTTGGGGTCTCATCGAGGACTTAAATGGAATGATATACGG 600  
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DB 661 CTTTCATTCCTCCAAAGCAGAAACGAAATGAGAGACAAATTTGAGCCAGAGTTGAA 720

QY 721 GAATAAGATGCTTTCATTGAAGAGTGCACATAGATTGAAATAACAGAAAATAGTTTT 780  
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QY 781 GAACAATAACATTTATGCAAGCTTACAACTATTCTTGAAGTACGAACAAGATAGA 840  
DB 781 GAACAATAACATTTATGCAAGCTTACAACTATTCTTGAAGTACGAACAAGATAGA 840

QY 841 ACTTCTCGTTTCAGCTTATTAATGATATAAAAAACACCTTGTTCCTA 888  
DB 841 ACTTCTCGTTTCAGCTTATTAATGATATAAAAAACACCTTGTTCCTA 888

RESULT 4  
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LOCUS Sequence 50 from patent US 6482414.  
DEFINITION  
ACCESSION AR254664  
VERSION AR254664.1 GI:27303685  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 891)  
AUTHORS Dowling,P.W. and Youngner,J.S.  
TITLE Cold-adapted equine influenza viruses  
JOURNAL Patent: US 6482414-A 50 19-NOV-2002;  
The University of Pittsburgh-of the Commonwealth System of Higher Education; Pittsburgh, PA

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source Location/Qualifiers  
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/organism="unknown"  
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Query Match 99.8%; Score 886.4; DB 6; Length 891;  
Best Local Similarity 99.9%; Pred. No. 6.9e-209;  
Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 AGCAAAAGCAGGCTGACAAAACATATGATTCACACCTGTGTCAAGCTTTCAAGTAG 60

QY 61 ACTGTTTCTTTGGCATGTCGCAAAACGATTTGCAGACCAAGAACTGGGTGATGCCCAT 120  
DB 61 ACTGTTTCTTTGGCATGTCGCAAAACGATTTGCAGACCAAGAACTGGGTGATGCCCAT 120

QY 121 TCCTTGACCGGCTTCGCGAGACGAGAGTCCCTTAAAGGAAGAGGTAGCACTCTTGTC 180  
DB 121 TCCTTGACCGGCTTCGCGAGACGAGAGTCCCTTAAAGGAAGAGGTAGCACTCTTGTC 180

QY 181 TGCACATCGAAGCAGCACTCTGTCAGGAAGCAGATAGTGAGCAGATCTTGGAGAGG 240  
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DB 301 ACATGACTCTTGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCAAGCAAGAAAGTAA 360

QY 361 CAGGCTCCCTATGATAGATGAGCAGGCAATCATGATAGAAACATCATCTTTAAAG 420  
DB 361 CAGGCTCCCTATGATAGATGAGCAGGCAATCATGATAGAAACATCATCTTTAAAG 420

QY 421 CAACCTTTAGTGTGATTTTCGAAGGCTCGAGACACTAACTACTTACCTAGAGCTTCACCG 480  
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QY 481 AAGAGGAGCAGTCTGTTGGGAAATTTCCACCATGCTTCTTCTTCCAGGACATCTAAATG 540  
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QY 541 AGGATGTCAAAAATGCAATTTGGGGTCTCATCGAGGACTTAAATGGAATGATATACGG 600  
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QY 601 TTAGAATCTCTGAACCTCTACAGAGATTCGCTTGGAGAGCAGTCTATGAGATGGAGAC 660  
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QY 661 CTTTCATTCCTCCAAAGCAGAAACGAAATGAGAGACAAATTTGAGCCAGAGTTGAA 720  
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Db 481 AAGAAGGAGCGTCTGGGGAATTTCCACATTCGCTTCTCTCCAGACATACATAATG 540  
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AR455539 AR455539 891 bp DNA linear PAT 20-FEB-2004  
LOCUS Sequence 50 from patent US 6685946.  
DEFINITION AR455539  
ACCESSION AR455539  
VERSION AR455539.1 GI:42690359  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 891)  
AUTHORS Dowing, P.W. and Youngner, J.S.  
TITLE Cold-adapted equine influenza viruses  
JOURNAL Patent: US 6685946-A 50 03-FEB-2004;  
The University of Pittsburgh-of the Commonwealth System of Higher Education: Pittsburgh, PA

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source Location/Qualifiers  
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ORIGIN  
Query Match 99.8%; Score 886.4; DB 6; Length 891;  
Best Local Similarity 99.9%; Pred No. 6.9e-209;  
Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCAAGCAGGCTGACAAACATATGATTCACACTGTGCAAGCTTTCAGGTAG 60  
Db 1 AGCAAGCAGGCTGACAAACATATGATTCACACTGTGCAAGCTTTCAGGTAG 60  
Qy 61 ACTGTTTCTTGGCATGTCGCAACGATTCGACCAAGCACTGGGTGATGCCCAT 120  
Db 61 ACTGTTTCTTGGCATGTCGCAACGATTCGACCAAGCACTGGGTGATGCCCAT 120  
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Qy 241 AATCAGATGAGGCACTTAAATAGCACTTGTCTCTGCTTCCAGCTTCACTTAACTG 300  
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Qy 481 AAGAAGGAGCAGTCTGTTGGCGAAATTTCCACCATTCCTCTTCCAGACATCTAATG 540  
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ACCESSION AX225022.1 GI:15555095  
VERSION  
KEYWORDS  
SOURCE Equine influenza virus H3N8  
ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
Influenzavirus A.

REFERENCE 1  
AUTHORS Dowing, P.W. and Youngner, J.S.  
TITLE Cold-adapted equine influenza viruses  
JOURNAL Patent: WO 0160849-A 32 23-AUG-2001;  
UNIV. OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION (US)

FEATURES  
source Location/Qualifiers  
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ORIGIN	Query Match	99.8%; Score 886.4; DB 6; Length 891;	
	Best Local Similarity	99.9%; Pred. No. 6.9e-209;	
	Matches 887; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1	AGCAAAAGCAGGGTGCACAAAACATAATGATTCACACACTGTGTCAAGCTTTTCAGGTAG	60
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Qy	61	ACTGTTTCTTGGCATCTCGCCAGACGATTTGACAGCCAGACCTGGGTGATGCCCAT	120
Db	61	ACTGTTTCTTGGCATCTCGCCAGACGATTTGACAGCCAGACCTGGGTGATGCCCAT	120
Qy	121	TCCTTGACCGGCTTCGCGAGACGAGAGTCCCTAAAGAGAGAGGTAGCACTCTTGTC	180
Db	121	TCCTTGACCGGCTTCGCGAGACGAGAGTCCCTAAAGAGAGAGGTAGCACTCTTGTC	180
Qy	181	TGACATCGAAACAGCCACTCTGCGAGAGAGAGAGTGTGAGAGAGTCTTGAGAGG	240
Db	181	TGACATCGAAACAGCCACTCTGCGAGAGAGAGAGTGTGAGAGAGTCTTGAGAGG	240
Qy	241	AATCAGATGAGCACTTAAATGACCAATTCCTCTGTTCTCTGCTTCAAGCTTAACTG	300
Db	241	AATCAGATGAGCACTTAAATGACCAATTCCTCTGTTCTCTGCTTCAAGCTTAACTG	300
Qy	301	ACATGACTCTTGATGAGATGTCAAGAGAGTGGTTCATGCTCATGCCCAAGCAGAGAAAT	360
Db	301	ACATGACTCTTGATGAGATGTCAAGAGAGTGGTTCATGCTCATGCCCAAGCAGAGAAAT	360
Qy	361	CAGGCTCCCTATGTATAGAGATGACACGAGCAATCATGAGTAAAGACATCATCTTAAAG	420
Db	361	CAGGCTCCCTATGTATAGAGATGACACGAGCAATCATGAGTAAAGACATCATCTTAAAG	420
Qy	421	CAAACTTTAGTGTGATTTTGGAGAGTTCACCAATTCACCAATTCACCAATTCACCAAT	480
Db	421	CAAACTTTAGTGTGATTTTGGAGAGTTCACCAATTCACCAATTCACCAATTCACCAAT	480
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Qy	541	AGGATGTCAAAATGCAATTTGGGCTCTCATCGAGAGTTCACCAATTCACCAATTCACCAAT	600
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Qy	601	TTAGAAATCTGAAATCTTACAGAGATTCGTTGAGAGAGTTCACCAATTCACCAATTCACCAAT	660
Db	601	TTAGAAATCTGAAATCTTACAGAGATTCGTTGAGAGAGTTCACCAATTCACCAATTCACCAAT	660
Qy	661	CTTCATTCCTCCAAAGCAGAAACGAAATTCGAGAGAGTTCACCAATTCACCAATTCACCAAT	720
Db	661	CTTCATTCCTCCAAAGCAGAAACGAAATTCGAGAGAGTTCACCAATTCACCAATTCACCAAT	720
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Qy	781	GAACAAATACCAATTTATGAGAGTTCACCAATTCACCAATTCACCAATTCACCAAT	840
Db	781	GAACAAATACCAATTTATGAGAGTTCACCAATTCACCAATTCACCAATTCACCAAT	840
Qy	841	ACTTTCTGCTTTCAGCTTATTTAATGATTAAGAGAGTTCACCAATTCACCAATTCACCAAT	888
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RESULT 7  
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LOCUS  
DEFINITION  
AR254666  
ACCESSION  
VERSION  
AR254666  
Sequence 53 from patent US 6482414.  
AR254666.1 GI:27303687

KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 888)	
AUTHORS	Dowling P.W. and Youngner J.S.	
TITLE	Cold-adapted equine influenza viruses	
JOURNAL	Patent: US 6482414-A 53 19-NOV-2002;	
	The University of Pittsburgh-of the Commonwealth System of Higher	
	Education; Pittsburgh, PA	
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	Query Match	99.6%; Score 884.4; DB 6; Length 888;
	Best Local Similarity	99.9%; Pred. No. 2.2e-208;
	Matches 885; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Qy	3	CAAAAGCAGGGTGCACAAAACATAATGATTCACACACTGTGTCAAGCTTTTCAGGTAGAC 62
Db	1	CAAAAGCAGGGTGCACAAAACATCATGGATTCACACACTGTGTCAAGCTTTTCAGGTAGAC 60
Qy	63	TGTTTCTTTTGCATGTCCGCAACGATTTTCAGACCAAGAACTGGGTGATGCCCATTC 122
Db	61	TGTTTCTTTTGCATGTCCGCAACGATTTTCGACCAAGAACTGGGTGATGCCCATTC 120
Qy	123	CTTGACCGGCTTCGCGAGACGAGAGTCCCTTAAAGAGAGAGGTGTGAGACTCTTGTTGCTG 182
Db	121	CTTGACCGGCTTCGCGAGACGAGAGTCCCTTAAAGAGAGAGGTGTGAGACTCTTGTTGCTG 180
Qy	183	GACATCGAAACAGCCACTCTGCGAGGAGAAAGCAGATGATGAGAGAGAGTCTTGGAGAGGAA 242
Db	181	GACATCGAAACAGCCACTCTGCGAGGAGAAAGCAGATGATGAGAGAGAGTCTTGGAGAGGAA 240
Qy	243	TCAGATGAGGCACTTAAATGACCAATTCCTGCTCTGCTTTCACGCTACTTAACTGAC 302
Db	241	TCAGATGAGGCACTTAAATGACCAATTCCTGCTCTGCTTTCACGCTACTTAACTGAC 300
Qy	303	ATGACTCTTTGATGAGATGTCAAGAGACTGGTTTCATGCTCATGCCCAAGCAGAGAAATGACA 362
Db	301	ATGACTCTTTGATGAGATGTCAAGAGACTGGTTTCATGCTCATGCCCAAGCAGAGAAATGACA 360
Qy	363	GGCTCCCTATGTATAAGAAATGAGACAGGCAATCATGGAATGAAGAAATCATATTAAGACA 422
Db	361	GGCTCCCTATGTATAAGAAATGAGACAGGCAATCATGGAATGAAGAAATCATATTAAGACA 420
Qy	423	AACCTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATATCTTCTAGAGGCTTTCACCGAA 482
Db	421	AACCTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATATCTTCTAGAGGCTTTCACCGAA 480
Qy	483	GAAAGAGCAGTCTGTTGGCGAAATTTCAACATTTGCTCTCTTCCAGGACATATTAATGAG 542
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Qy	543	GATGTCAAAAATGCAATTTGGGCTTCCTCATCGGAGACTTAAATGGAATGATTAATGAGTT 602
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Db	601	AGATCTCTGAAACTCTACAGAGATTCGCTTCGAGAGACGAGTCTATGAGAAATCGGAGACCT 660
Qy	663	TCATTCCTCCAAAGCAGAAACGAAATTCGAGAGAGCAATTTGAGCCAGAGTCTTTGAAGA 722
Db	661	TCATTCCTCCAAAGCAGAAACGAAATTCGAGAGAGCAATTTGAGCCAGAGTCTTTGAAGA 720
Qy	723	AATAAGATGTTTGTATTGAAGAGTGGCAGATAGATTGAAAAATACAGAAAAATAGTTTTGA 782
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LOCUS AR455541 888 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 53 from patent US 6685946.  
ACCESSION AR455541  
VERSION AR455541.1 GI:42690361  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 888)  
AUTHORS Dowling, P.W. and Youngner, J.S.  
TITLE Cold-adapted equine influenza viruses  
JOURNAL Patent: US 6685946-A 53 03-FEB-2004;  
The University of Pittsburgh-of the Commonwealth System of Higher Education; Pittsburgh, PA

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ORIGIN  
Query Match 99.6%; Score 884.4; DB 6; Length 888;  
Best Local Similarity 99.9%; Pred. No. 2.2e-208;  
Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAAAGCAGGGTGACAAAACATATGATTCACACTGTGTCAAGCTTTCAGGTAGAC 62  
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Qy 123 CTTGACCGGCTTCGCGAGACCAAGTCCCTAAAGAGAGAGTAGACTCTTGTCTG 182  
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Qy 183 GACATCGAAGACGCACTCGTCGAGGAAGCAGATAGTGAGCAGATTTCTGGAAGGAA 242  
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Db 301 ATGACTCTTGATGATGTCAAGAGCTGGTTCATGCTCAGTCCCGCAGAGAAAGTAACA 360

Qy 363 GGCTCCCTATGATATAGATGGAACGAGGCACTCATGATTAAGACATCATCTAAAGCA 422  
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Qy 843 TTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTA 888  
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RESULT 9  
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LOCUS AX225025 888 bp DNA linear PAT 10-SEP-2001  
DEFINITION Sequence 35 from Patent WO0160849.  
ACCESSION AX225025  
VERSION AX225025.1 GI:15555098  
KEYWORDS Equine influenza virus H3N8  
SOURCE Equine influenza virus H3N8  
ORGANISM Viruses; sRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.

REFERENCE 1  
AUTHORS Dowling, P.W. and Youngner, J.S.  
TITLE Cold-adapted equine influenza viruses  
JOURNAL Patent: WO 0160849 A 35 23-AUG-2001;  
UNIV. OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION (US)

FEATURES  
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ORIGIN  
Query Match 99.6%; Score 884.4; DB 6; Length 888;  
Best Local Similarity 99.9%; Pred. No. 2.2e-208;  
Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAAAGCAGGGTGACAAAACATATGATTCACACTGTGTCAAGCTTTCAGGTAGAC 62  
Db 1 CAAAGCAGGGTGACAAAACATATGATTCACACTGTGTCAAGCTTTCAGGTAGAC 60

Qy 63 TGTTCCTTTGGCATGTCCGCAACGATTTGACAGCAAGACTGGGTGATGCCCATTC 122  
Db 61 TGTTCCTTTGGCATGTCCGCAACGATTTGACAGCAAGACTGGGTGATGCCCATTC 120

Qy 123 CTTGACCGGCTTCGCGAGACCAAGTCCCTAAAGAGAGAGTAGACTCTTGTCTG 182  
Db 121 CTTGACCGGCTTCGCGAGACCAAGTCCCTAAAGAGAGAGTAGACTCTTGTCTG 180

Qy 183 GACATCGAAGACGCACTCGTCGAGGAAGCAGATAGTGAGCAGATTTCTGGAAGGAA 242  
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QY 363 GGCTCCTATGTATGAAGATGGACAGGCAATCATGGATAGAAACATCATCTTAAAGCA 422  
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 QY 663 TCATTCCTCCAAAGCAGAAACGAAATGGAGAGCAATTCGAGCCAGAGTTTGA 722  
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 Db 781 ACAATAACATTTATGCAAGCTTACAACATTTGCTTGAAGTAGAACAAGAGATAAGAAC 840  
 QY 843 TTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCTTTGTTCTA 888  
 Db 841 TTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCTTTGTTCTA 886

RESULT 10  
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 DEFINITION protein, complete cds.  
 ACCESSION M80973  
 VERSION M80973.1 GI:348780  
 KEYWORDS  
 SOURCE Influenza A virus  
 ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 Influenzavirus A.  
 REFERENCE 1 (bases 1 to 890)  
 AUTHORS Kawaoka, Y., Gorman, O.T., Ito, T., Wells, K., Denis, R.O.,  
 Castucci, M.R., Donatelli, I., and Webster, R.G.  
 TITLE Influence of host species on the evolution of the nonstructural  
 (NS) gene of influenza A viruses  
 JOURNAL Virus Res. 55 (2), 143-156 (1998)  
 PUBMED 9725667  
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Query Match 99.1%; Score 880; DB 13; Length 890;  
 Best Local Similarity 99.4%; Pred. No. 2.7e-207;  
 Matches 883; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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 QY 241 ANTACATGAGGACCTTAAATGATGACCATTCCTGTTCTGCTTCCAGCTACTTAACG 300  
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 Db 421 CAACTTTAGTGTGATTTTGAAGGCTGGAGACACTAACTACTTACAGGCTTCCACG 480  
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 QY 841 ACTTTCCTGTTTCAGCTTATTTAATGATAAAAAACACCTTTGTTCTA 888  
 Db 841 ACTTTCCTGTTTCAGCTTATTTAATGATAAAAAACACCTTTGTTCTA 888

RESULT 11  
 FLANSEQUE  
 LOCUS Influenza A virus isolate A/equine/Kentucky/76 nonstructural  
 DEFINITION protein, complete cds.  
 ACCESSION M80971

Db	541	AGGATGTCAAAATGCAATTGGGGCTCTCATCGAGGACTTAAATGGAATGATAACACAG	600
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Qy	661	CTTCAATTCCTCCAAAGCAGAAACGAAATGCGAGACACATTTGAGCAGAAATTTGAA	720
Db	661	CTTCAATTCCTCCAAAGCAGAAACGAAATGCGAGACACATTTGAGCAGAAATTTGAA	720
Qy	721	GAATAAGATGGTTGATTCGAAGAGTGGACATAGATTCGAAATACAGAAATAGTTTT	780
Db	721	GAATAAGATGGTTGATTCGAAGAGTGGACATAGATTCGAAATACAGAAATAGTTTT	780
Qy	781	GAACAAATACATTTATGCAAGCGCTTACAATTCCTTGAAGTACAGACAGATAAGA	840
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DEFINITION			
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RESULT 14
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LOCUS
DEFINITION
Influenza A virus isolate A/equine/New York/49/73 nonstructural
protein, complete cds.
ACCESSION
M80976
VERSION
M80976.1
KEYWORDS
GI:348772
SOURCE
Influenza A virus
ORGANISM
Influenza A virus
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
REFERENCE
1 (bases 1 to 890)
Kawaoka,Y., Gorman,O.T., Ito,T., Wells,K., Donis,R.O.,
Castucci,M.R., Donatelli,I. and Webster,R.G.
Influence of host species on the evolution of the nonstructural
(NS) gene of influenza A viruses
Virus Res. 55 (2), 143-156 (1998)
PUBLISHED
9725667
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Location/Qualifiers
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/mol_type="unassigned RNA"
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KKRMARTIESEV"

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Db 241 AGTCAGATGAGGCACTTAAATGACATTCGCTCTGTCTGCTTTCAGCTTAACTG 300
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RESULT 15
AY855345
LOCUS
DEFINITION
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protein gene, complete cds.
ACCESSION
AY855345
VERSION
AY855345.1
KEYWORDS
GI:60547114
SOURCE
Influenza A virus (A/equine/Kentucky/5/02 (H3N8))
ORGANISM
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
REFERENCE
1 (bases 1 to 890)
Quinlivan,M., Zamarin,D., Garcia-Sastre,A., Cullinane,A.,
Chambers,T. and Palese,P.
Attenuation of equine influenza viruses through truncations of the
NS1 protein
Unpublished
2 (bases 1 to 890)
Quinlivan,M., Zamarin,D., Garcia-Sastre,A., Cullinane,A.,
Chambers,T. and Palese,P.
Direct Submission
Submitted (14-DEC-2004) Microbiology, Mount Sinai School of
Medicine, 1 Gustave Levy Place, New York, NY 10029, USA
JOURNAL
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	Matches 874; Conservative	0; Mismatches 14; Indels	0; Gaps	0;
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QY	121	TCCTTGACCGGCTTCGCGAGACCAAGATCCCTAAAGGAGAGAGTAGCAGCTCTTTGGTC	180	
DB	121	TCCTTGACCGGCTTCGCGAGACCAAGATCCCTAAAGGAGAGAGTAGCAGCTCTTTGGTC	180	
QY	181	TGGACATCGAAACAGCCACTCGTCAGGAAAGCAGATAGTGGAGCAGATTCGGAAGAGG	240	
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QY	241	AATCAGATAGGCACTTAAATGACCATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	300	
DB	241	AATCAGATAGGCACTTAAATGACCATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	300	
QY	301	ACATGACTCTTGATGAGATGTCGAAGACATGGTTTCATGCTCATGCCCAAGCAGAAAGTAA	360	
DB	301	ACATGACTCTTGATGAGATGTCGAAGACATGGTTTCATGCTCATGCCCAAGCAGAAAGTAA	360	
QY	361	CAGGCTCCTCTGTATATAGAAATGGACAGGCAATCATGGATAAGAACATCATCTTAAAG	420	
DB	361	CAGGCTCCTCTGTATATAGAAATGGACAGGCAATCATGGATAAGAACATCATCTTAAAG	420	
QY	421	CAAACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCG	480	
DB	421	CAAACTTTAGTGTGATTTTCGAAAGGCTGGAAACACTAATACTACTTAGAGCCTTCACCG	480	
QY	481	AAGAAGAGCAGTCGTTGGCGAAATTTCCACATTCCTCTCTCTCTCTCTCTCTCTCTCT	540	
DB	481	AAGAAGAGCAGTCGTTGGCGAAATTTCCACATTCCTCTCTCTCTCTCTCTCTCTCTCT	540	
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QY	661	CTTCATTCCTCCCAAGCAGAAACGAAATGGAGAGACATTCGCGCAGAGTTTGA	720	
DB	661	CTTCATTCCTCCCAAGCAGAAATGAAATGGAGAGACATTCGCGCAGAGTTTGA	720	
QY	721	GAAATAGATGGTGTGATGAGAGAGTGGGACATAGATTGAAATACAGAAATAGTTTTT	780	
DB	721	GAAATAGATGGTGTGATGAGAGAGTGGGACATAGATTGAAATACAGAAATAGTTTTT	780	
QY	781	GAACAAATACATTTATGCAAGCCTTACAACTATTGCTTGAAGTAGAACAGAGATAAGA	840	
DB	781	GAACAAATACATTTATGCAAGCCTTACAACTATTGCTTGAAGTAGAACAGAGATAAGA	840	
QY	841	ACTTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTTTCTTA	888	

Db 841 ACTTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTTTCTA 888

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Job time : 4574.81 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 23:54:43 ; Search time 557.673 Seconds  
(without alignments)  
10612.397 Million cell updates/sec

Title: US-10-734-373-57  
Perfect score: 888  
Sequence: 1 agcaaaagcagggtagacaaa.....aaaaaacacctgtttcta 888

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues  
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001as.\*  
5: Geneseq2001bs.\*  
6: Geneseq2002as.\*  
7: Geneseq2002bs.\*  
8: Geneseq2003as.\*  
9: Geneseq2003bs.\*  
10: Geneseq2003qs.\*  
11: Geneseq2003ds.\*  
12: Geneseq2004as.\*  
13: Geneseq2004bs.\*  
14: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	888	100.0	888	4	AAD15681 Equine in
2	886.4	99.8	891	4	AAD15678 Equine in
3	884.4	99.6	888	4	AAD15679 Equine in
4	744	83.8	890	2	AAX82197 Influenza
5	744	83.8	890	12	ADOL15247 Influenza
6	742.4	83.6	890	14	ADW44527 Influenza
7	737.6	83.1	890	6	AAD37061 Influenza
8	731.2	82.3	1146	3	AAA75003 Nucleotid
9	729.6	82.2	890	2	AAQ22332 RNA (+),
10	707.2	79.6	890	6	ABA93942 Influenza
11	706.4	79.5	906	4	AHH77932 Nucleotid
12	692.8	78.0	824	14	ADY62118 Non-struc
13	685	77.1	693	2	AAT37435 Influenza
14	684.8	77.1	824	14	ADY62117 Influenza
15	463.4	52.2	468	4	AAD15680 Equine in
16	286.4	32.3	402	6	ABA93943 Influenza
17	213.4	24.0	6010	2	AAT59676 Plasmid P
18	213	24.0	596	2	AAQ20237 Encodes V
19	212.8	24.0	918	2	AAQ47361 Sequence

20	212.8	24.0	918	2	AAQ70190 Sequence
21	212.8	24.0	918	2	AAQ70208 Sequence
22	212	23.9	453	2	AAT95097 Porcine s
23	212	23.9	453	6	AAD27035 Influenza
24	212	23.9	690	2	AAQ47362 Sequence
25	212	23.9	690	2	AAQ70191 Sequence
26	212	23.9	690	2	AAQ70209 Sequence
27	212	23.9	524	2	AAQ40402 Coding re
28	212	23.9	524	2	AAQ47364 Sequence
29	212	23.9	924	2	AAQ70195 Sequence
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36	211.6	23.8	729	2	AAQ04073 Coding re
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43	210.4	23.7	1020	2	AAQ38090 NS1-ZQ1 f
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ALIGNMENTS

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AC AAD15681;  
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XX  
DT 15-NOV-2001 (first entry)  
XX Equine influenza virus H3N8 neicaiNS888 DNA.  
XX Equine influenza virus; ei; cold adaptation; temperature sensitivity;  
KW vaccine; neicaiNS888 DNA; PeicaiNS230 protein; ds.  
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OS Equine influenza virus H3N8.  
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XX WO200160849-A2.  
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PD 23-AUG-2001.  
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PF 16-FEB-2001; 2001WO-US005048.  
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PR 16-FEB-2000; 2000US-00506286.  
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XX (UYPI-) UNIV PITTSBURGH.  
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XX Dowling PW, Youngner JS;  
XX WPI: 2001-522584/57.  
XX P-PSDB; AAE09029.  
XX Novel isolated equine influenza virus (wild-type and cold-adapted) proteins and viruses containing nucleic acid molecules encoding the proteins, which are useful for protecting animals from influenza virus

PT	infections.
XX	Claim 2; Page 75-76; 172pp; English.
PS	
XX	The patent discloses cold-adapted equine influenza viruses and
CC	reassortant influenza A viruses comprising at least one genome segment of
CC	such an equine influenza virus, wherein the equine influenza virus genome
CC	segment confers at least one identifying phenotype of the cold-adapted
CC	equine influenza virus, such as cold adaptation, temperature sensitivity,
CC	equine influenza virus attenuation. The viruses are useful for
CC	dominant interference or attenuation of influenza viruses. They are
CC	protecting animals from diseases caused by influenza viruses. (61)
CC	also used as vaccines. The present sequence is equine influenza (61)
CC	virus H3N8 neilcal (cold adapted) NS888 DNA encoding PeIcalNS230 protein
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SQ	Sequence 888 BP; 300 A; 173 C; 198 G; 217 T; 0 U; 0 Other;
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Matches 888; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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DB	721 GAAATAGAGATGGTTGATTTGAAGAGAGTCCGACATAGATTTGAAAAATTCAGAAATAGTTTT 780
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QY 61 ACTGTTTCTTTGGGATGTCGCAAAACGATTTGCGAGACCAAGAACTGGGTGATGCCCAT 120  
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RESULT 3  
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 ID AAD15679 standard; DNA; 888 BP.  
 AC AAD15679;  
 XX  
 DT 15-NOV-2001 (first entry)  
 DE Equine influenza virus H3N8 neiwt3NS888 DNA.  
 XX  
 KW Equine influenza virus; ei; cold adaptation; temperature sensitivity;  
 XX vaccine; neiwt3NS888 DNA; ds.  
 OS Equine influenza virus H3N8.  
 XX

PN WO200150849-A2.  
 XX 23-AUG-2001.  
 XX 16-FEB-2001; 2001WO-US005048.  
 XX 16-FEB-2000; 2000US-00506286.  
 XX (UYPI-) UNIV PITTSBURGH.  
 XX Dowling PW, Youngner JS;  
 XX WPI; 2001-522584/57.  
 XX Novel isolated equine influenza virus (wild-type and cold-adapted)  
 XX proteins and viruses containing nucleic acid molecules encoding the  
 XX proteins, which are useful for protecting animals from influenza virus  
 XX infections.  
 XX Claim 2; Page 74; 172pp; English.  
 XX The patent discloses cold-adapted equine influenza viruses and  
 XX reasortant influenza A viruses comprising at least one genome segment of  
 XX such an equine influenza virus, wherein the equine influenza virus genome  
 XX segment confers at least one identifying phenotype of the cold-adapted  
 XX equine influenza virus, such as cold adaptation, temperature sensitivity,  
 XX dominant interference or attenuation. The viruses are useful for  
 XX protecting animals from diseases caused by influenza viruses. They are  
 XX also used as vaccines. The present sequence is an equine influenza (ei)  
 XX virus H3N8 neiwt3 (wild type) NS888 DNA  
 XX  
 SQ Sequence 888 BP; 298 A; 174 C; 198 G; 218 T; 0 U; 0 Other;  
 Query Match 99.6%; Score 884.4; DB 4; Length 888;  
 Best Local Similarity 99.9%; Pred. No. 9e-238;  
 Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 CAAGAAGGAGGTCGCAAAACATATGGAATCCAACTGTCAGCTTTCAGGTAGAC 62  
 Db 1 CAAGAAGGAGGTCGCAAAACATATGGAATCCAACTGTCAGCTTTCAGGTAGAC 60  
 QY 63 TGTGTTCTTTGGCATGTCCGCAACGATTTGCGAGACCAAGCACTGGGTGATGCCCATTC 122  
 Db 61 TGTGTTCTTTGGCATGTCCGCAACGATTTGCGAGACCAAGCACTGGGTGATGCCCATTC 120  
 QY 123 CTTGACCGGCTTCCGCGAGACCAAGATCCCTAAAGGAAGAGGTAGCACTCTTGCTG 182  
 Db 121 CTTGACCGGCTTCCGCGAGACCAAGATCCCTAAAGGAAGAGGTAGCACTCTTGCTG 180  
 QY 183 GACATCGAAACAGCCACTCGTGCGAGGAAAGCAGATAGTGGAGCAGATTTGGAAGAGAA 242  
 Db 181 GACATCGAAACAGCCACTCGTGCGAGGAAAGCAGATAGTGGAGCAGATTTGGAAGAGAA 240  
 QY 243 TCAGATGAGGCACTTAAATGACCATTTGCTCTGTTCTGCTTCCAGCTACTTAACTGAC 302  
 Db 241 TCAGATGAGGCACTTAAATGACCATTTGCTCTGTTCTGCTTCCAGCTACTTAACTGAC 300  
 QY 303 ATGACTCTTGATGAGATGTCAGAGACTGTTTCATGCTCATGCCCAAGCAGAAAGTAA 362  
 Db 301 ATGACTCTTGATGAGATGTCAGAGACTGTTTCATGCTCATGCCCAAGCAGAAAGTAA 360  
 QY 363 GGCTCCCTATGATTAAGATGGAAGTGGACCAAGCAATCATGATAGAACATCATACTTAAAGCA 422  
 Db 361 GGCTCCCTATGATTAAGATGGAAGTGGACCAAGCAATCATGATAGAACATCATACTTAAAGCA 420  
 QY 423 AACTTTAGTGTGATTTTCGAAGGCTGGAGACACTAATACTACTTTAGAGCCTTCACCGAA 482  
 Db 421 AACTTTAGTGTGATTTTCGAAGGCTGGAGACACTAATACTACTTTAGAGCCTTCACCGAA 480  
 QY 483 GAAGAGAGCAGTCTGTTGGCGAAATTTCAACATTTGCCCTCTCTTCCAGACATATAATGAG 542  
 Db 481 GAAGAGAGCAGTCTGTTGGCGAAATTTCAACATTTGCCCTCTCTTCCAGACATATAATGAG 540

QY 543 GATGTCAAAATCGATTCGGCTCCTCATCGGAGACTTAAATGAATGATTAACGGTT 602  
DB 541 GATGTCAAAATCGATTCGGCTCCTCATCGGAGACTTAAATGAATGATTAACGGTT 600  
QY 603 AGAATCTCTGAACTTACAGATTCGCTTGGAGAGCAGTCATGAGATGGGAGACCT 662  
DB 601 AGAATCTCTGAACTTACAGATTCGCTTGGAGAGCAGTCATGAGATGGGAGACCT 660  
QY 663 TCATTCCTCCAAAGCGAAACGAAATGAGAGAGCAATTCAGCCAGAGTTTGAAGA 722  
DB 661 TCATTCCTCCAAAGCGAAACGAAATGAGAGAGCAATTCAGCCAGAGTTTGAAGA 720  
QY 723 AATAAGATGGTTGATTCAAGAAGTGGGACATAGATTCGAAATACAGAAATAGTTTGA 782  
DB 721 AATAAGATGGTTGATTCAAGAAGTGGGACATAGATTCGAAATACAGAAATAGTTTGA 780  
QY 783 ACAATAAATCATTTATGCAAGCCTTCAACTATTGCTTGAAGTAGAACAGAGATAGAAC 842  
DB 781 ACAATAAATCATTTATGCAAGCCTTCAACTATTGCTTGAAGTAGAACAGAGATAGAAC 840  
QY 843 TTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTCTA 888  
DB 841 TTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTCTA 886

RESULT 4  
AX82197  
ID AX82197 standard; DNA; 890 BP.  
AC AX82197;  
XX  
XX  
XX 18-AUG-1999 (first entry)  
XX  
XX Influenza virus NS protein gene sequence.  
XX  
XX Cold-adapted influenza virus; passage culture; PB2 protein; PB1 protein;  
XX PA protein; NP protein; M protein; NS protein; temperature sensitivity;  
XX vaccine; flu; influenza; ss.  
XX  
XX Influenza virus.  
XX  
XX WO928445-A1.  
XX  
XX 10-JUN-1999.  
XX  
XX 30-NOV-1998; 98WO-KR000384.  
XX  
XX 29-NOV-1997; 97KR-00064854.  
XX  
XX (CHET-) CHEIL JEDANG CORP.  
XX  
XX Seong BL, Lee KH, Yoon JW, Kim SJ, Cheoun KH, Kim J, Kim HG;  
XX  
XX WPI; 1999-385377/32.  
XX  
XX Cold-adapted influenza viruses useful for the production of protective  
XX vaccines against flu.  
XX  
XX Claim 4; Page 58; 62pp; English.  
XX  
XX The invention relates to cold-adapted influenza viruses prepared by  
XX passage culture of A/X-31, B/Yamagata/16/88 or B/Lee/40 viruses at low  
XX temperatures. A cDNA gene of cold-adapted influenza virus H5N1-A101 can  
XX be selected from a group consisting of PB2 protein gene, PB1 protein  
XX gene, PA protein gene, NP protein gene, M protein gene and NS protein  
XX gene (AX82192-X82197). The method is useful for the production of cold-  
XX adapted influenza virus that exhibit temperature sensitivity and can be  
XX actively grown in fertilized eggs. The virus is useful for vaccines for  
XX protection against 'flu. Live vaccines containing cold-adapted viruses  
XX have several advantages over killed vaccines. It can prevent reduction of  
XX immunogenicity, which may occur in the killed vaccine where antigenic  
XX proteins would be denatured at its inactivation. It can also avoid  
XX hypersensitivity due to the prolonged administration of heterologous  
XX

proteins. It promotes the immunity by inducing IgA and it can be  
administered into a spray formulation via nasal cavity and thus its  
application is convenient for children. It is able to inhibit the growth  
of the wild-type virus and thus its therapeutic effect can be expected.  
The present sequence represents the influenza virus NS protein gene  
Sequence 890 BP; 283 A; 179 C; 215 G; 213 T; 0 U; 0 Other;  
Query Match 83.8%; Score 744; DB 2; Length 890;  
Best Local Similarity 89.9%; Pred. No. 2.5e-198;  
Matches 798; Conservative 0; Mismatches 90; Indels 0; Gaps 0;  
QY 1 AGCAAAAGCAGGGTGACAAAACACATAATGGATTCCACACTGTGTCAAGCTTTTCAGGTAG 60  
DB 1 AGCAAAAGCAGGGTGACAAAACACATAATGGATTCCACACTGTGTCAAGCTTTTCAGGTAG 60  
QY 61 ACTGTTTCTTTTGGCATGTCGCAACAGATTTGAGAGCAAGAACTGGGTGTATGCCCAT 120  
DB 61 ATTGCTTCTTTTGGCATGTCGCAACAGATTTGAGAGCAAGAACTGGGTGTATGCCCAT 120  
QY 121 TCCTTCAGCGGCTTCGCGAGACAGAACTCCCTTAAAGGAAGAGGTAGTCTTGGTC 180  
DB 121 TCCTTCAGCGGCTTCGCGAGACAGAACTCCCTTAAAGGAAGAGGTAGTCTTGGTC 180  
QY 181 TGGACATCGAAGACAGCCACTCTGTCAGGAAACAGATAGTGGAGCAGATTTCTGGAGAGG 240  
DB 181 TGGACATCGAAGACAGCCACTCTGTCGAGAAACAGATAGTGGAGCAGATTTCTGAAAGAG 240  
QY 241 AATCAGATGAGGCACTTAAATGACCATTTGCTCTCTGTTTCAAGCTACTTAACTG 300  
DB 241 AATCCGATGAGGCACTTAAATGACCATTTGCTCTCTGTTTCAAGCTACTTAACTG 300  
QY 301 ACATGACTCTTATGAGATGTCAGAGACTGAGAGCTGGTTCATCTCATGCCCAAGCAAGTAA 360  
DB 301 ACATGACTCTTATGAGATGTCAGAGACTGAGAGCTGGTTCATCTCATGCCCAAGCAAGTAA 360  
QY 361 CAGGCTCCCTATGATTAAGATGACAGGCACTCATGATAGCAAGCAATCATACTTAAAG 420  
DB 361 CAGGCTCCCTATGATTAAGATGACAGGCACTCATGATAGCAAGCAATCATACTTAAAG 420  
QY 421 CAAACTTTAGTGTGATTTTCAAGAGCTTGGAGCACTTAATCTACTTTAGAGCCTTCAACCG 480  
DB 421 CAAACTTTAGTGTGATTTTCAAGAGCTTGGAGCACTTAATCTACTTTAGAGCCTTCAACCG 480  
QY 481 AAGAGGAGCAGCTGCTGGCGGAAATTTTCAACCTTGGAGCTTCTTCCAGGACATCTAATG 540  
DB 481 AAGAGGAGCAGCTGCTGGCGGAAATTTTCAACCTTGGAGCTTCTTCCAGGACATCTAATG 540  
QY 541 AGGATGTCAAAAATGCAATTTGGGGTCTCTCATCGGAGACTTAAATGAGATTAATACCG 600  
DB 541 AGGATGTCAAAAATGCAATTTGGGGTCTCTCATCGGAGACTTAAATGAGATTAATACCG 600  
QY 601 TTAGAAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGAGCAGTCTGAGATGGGAGAC 660  
DB 601 TTAGAAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGAGCAGTCTGAGATGGGAGAC 660  
QY 661 CTTTCATTCCTCCAAAGCAGAAACGAAATTTGAGAGAGAACTTGAAGCAGAGTTTGA 720  
DB 661 CTTTCATTCCTCCAAAGCAGAAACGAGAAATTTGAGAGAGAACTTGAAGCAGAGTTTGA 720  
QY 721 GAAATAAGATGTTGATTGAGAAAGTGGGACATAGATTGAAAAATACAGAAATAGTTTT 780  
DB 721 GAAATAAGATGTTGATTGAGAAAGTGGGACATAGATTGAAAAATACAGAAATAGTTTT 780  
QY 781 GAAATAAGATGTTGATTGAGAAAGTGGGACATAGATTGAAAAATACAGAAATAGTTTT 840  
DB 781 GAAATAAGATGTTGATTGAGAAAGTGGGACATAGATTGAAAAATACAGAAATAGTTTT 840  
QY 841 ACTTCTGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTCTA 888  
DB 841 ACTTCTGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTCTA 888

CC proteins. It promotes the immunity by inducing IgA and it can be  
CC administered into a spray formulation via nasal cavity and thus its  
CC application is convenient for children. It is able to inhibit the growth  
CC of the wild-type virus and thus its therapeutic effect can be expected.  
CC The present sequence represents the influenza virus NS protein gene  
XX  
SQ Sequence 890 BP; 283 A; 179 C; 215 G; 213 T; 0 U; 0 Other;

RESULT 5  
 ADOI5247  
 ID ADOI5247 standard; DNA; 890 BP.  
 XX AC ADOI5247;  
 XX DT 12-AUG-2004 (first entry)  
 XX DE Influenza virus non-structural protein ISDN 13426 DNA.  
 XX KW vaccine; T-cell epitope; antibody; B-cell receptor; CD40; CD28;  
 KW immune response; immunisation; antibacterial; virucide; antiparasitic;  
 KW fungicide; antidiabetic; cytostatic; bacterial antigen; virus antigen;  
 KW parasite antigen; fungal antigen; influenza virus; gene; ds.  
 XX OS Influenza virus.  
 XX PN W02004041866-A1.  
 XX PD 21-MAY-2004.  
 XX PF 03-NOV-2003; 2003WO-GB004738.  
 XX PR 05-NOV-2002; 2002GB-00025736.  
 XX PA (ADJU-) ADJUVANTIX LTD.  
 XX PI Heath A;  
 XX PF WPI; 2004-400648/37.  
 XX DR Vaccine composition for immunizing humans or animals against T-cell  
 PT independent antigens, e.g. bacteria, viruses, parasites or fungi,  
 PT comprises antibodies against B-cell receptor CD40 or CD28.  
 XX PS Disclosure; Fig 16; Sipp; English.  
 XX CC The present invention describes a vaccine composition (1) comprising a  
 CC conjugate comprising a carrier group having a T-cell epitope and an  
 CC adjuvant, where the adjuvant is an antibody, or its binding part, which  
 CC binds the B-cell receptor CD40 or CD28 and a second conjugate comprising  
 CC a second carrier group comprising a T-cell epitope and an antigen to  
 CC which an immune response is desired. Also described: (1) methods of  
 CC immunising an animal to an antigen; (2) an antibody obtained by the above  
 CC method, which binds the antigen part of the second conjugate; (3) a  
 CC method for preparing a hybridoma cell-line producing monoclonal  
 CC antibodies described above; and (4) a hybridoma-cell line obtained by the  
 CC above method. (1) has antibacterial, virucide, antiparasitic, fungicide,  
 CC antiaddictive and cytostatic activities, and can be used in vaccines. The  
 CC composition (1) and methods are useful for immunising humans or animals  
 CC against T-cell independent antigens, such as bacteria, viruses, parasites  
 CC or fungi. The present sequence represents an influenza virus nucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX SQ Sequence 890 BP; 283 A; 180 C; 215 G; 212 T; 0 U; 0 Other;  
 Query Match 83.8%; Score 744; DB 12; Length 890;  
 Best Local Similarity 89.9%; Pred. No. 2.5e-198;  
 Matches 798; Conservative 0; Mismatches 90; Indels 0; Gaps 0;  
 QY 1 AGCAAAAGCAGGCTGACAAACATATGATTCACACACTGTGTCAAGCTTTCAGGTAG 60  
 DB 1 AGCAAAAGCAGGCTGACAAACATATGATTCACACACTGTGTCAAGCTTTCAGGTAG 60  
 QY 61 ACTGTTTCTTCCGATGTCGCAAGAGTTTCAGACCAAGCACTGGGTGATGCCGAT 120  
 DB 61 ATTGCTTCTTCCGATGTCGCAAGAGTTTCAGACCAAGCACTGGGTGATGCCGAT 120  
 QY 121 TCCTTGACCGGCTTCCCGAGACCAAGAGTCCCTAAAGAGAGAGGTAGACTCTTGGTC 180  
 DB 121 TCCTTGATCGGCTTCCCGAGATCAGAAATCCCTTAAGAGAGAGGCGGAGTACTCTCGGTC 180  
 QY 181 TGGACATCGAAACAGCCACTCTGTGCAAGAAAGCAGATAGTGGAGCAGATTCTTGAAGAG 240

DB 181 TGGACATCGAAACAGCCACTCTGTGCAAGAGCAGATAGTGGAGCGGATTTCTGAAGAAG 240  
 QY 241 AATCAGATGAGGCACCTTAAATGACCATTTGCTCTGTTCCTGCTTCCCTACTTAACTG 300  
 DB 241 AATCCGATGAGGCACCTTAAATGACCATTTGCTCTGTTCCTGCTTCCCTACTTAACTG 300  
 QY 301 ACATGACTCTTGATGAGATGTCAGAGACTGTTTCATGCTCATGCTCCCAAGCAAGCTAA 360  
 DB 301 ACATGACTCTTGAGGAATGTCAAGGACTGTCTCATGCTCATGCTCCCAAGCAAGCTG 360  
 QY 361 CAGGCTCTTATGATTAAGAAATGAGCAGCAATCATGATTAAGAAACATCATCTTAAAG 420  
 DB 361 CAGGCTCTTATGATTAAGAAATGAGCAGCAATCATGATTAAGAAACATCATCTTAAAG 420  
 QY 421 CAACTTTAGTGTGATTTTCGAAAGGCTGAGAGACATAAATACTATTAGAGCTTTCACCG 480  
 DB 421 CGAATCTCAGTGTGATTTTTCGCGGCTGAGAGACTCTAAATATTGCTAAGGGCTTTCACCG 480  
 QY 481 AAGAAGGAGCAGTCTGTTGGCGAAATTTCAACATTTGCTTCTTCCAGGACATATAATG 540  
 DB 481 AAGAAGGAGCAGTCTGTTGGCGAAATTTTCACCAATTTGCTTCTTCCAGGACATATAATG 540  
 QY 541 AGGATGTCAAAAATGCAATTTGGGCTCTCATCGAGGACTTAAATGGAATGATAATACGG 600  
 DB 541 AGGATGTCAAAAATGCAATTTGGGCTCTCATCGAGGACTTAAATGGAATGATAATACAG 600  
 QY 601 TTAGAATCTCTGAAACTCTACAGAGATTGCTTGGAGAGCAGTCAATGAGATGGAGAC 660  
 DB 601 TTGAGTCTCTGAAACTCTACAGAGATTGCTTGGAGAGCAGTCAATGAGATGGAGAC 660  
 QY 661 CTTCATTCCTCCCAAGCAGACGAAATGAGAGCAATTTGAGCCAGAGTTTGA 720  
 DB 661 CTCCACTCACTCCAAACAGAAATGCGGGAACATTTAGTCTAGAGTTTGA 720  
 QY 721 GAATTAAGATGCTTCAATGAGAGTGGAGCAGTCAATGAGATGAAATACAGAAATAGTTT 780  
 DB 721 GAATTAAGATGCTTCAATGAGAGTGGAGCAGTCAATGAGATGAAATACAGAAATAGTTT 780  
 QY 781 GAACAAATACATTTATGCAAGCTTACAACTATTGCTTGAAGTAGAACAGAGATAAGA 840  
 DB 781 GAGCAAAATACATTTATGCAAGCTTACAACTATTGCTTGAAGTAGAACAGAGATAAGA 840  
 QY 841 ACTTCTGCTTTCAGCTTATTATTAAGTATAAAAAACACCTTGTGTTCTA 888  
 DB 841 ACTTCTGCTTTCAGCTTATTATTAAGTATAAAAAACACCTTGTGTTCTA 888  
 RESULT 6  
 ADW44527  
 ID ADW44527 standard; cDNA; 890 BP.  
 XX AC ADW44527;  
 XX DT 24-MAR-2005 (first entry)  
 XX DE Influenza A virus NS cDNA.  
 XX KW virucide; vaccine; gene therapy; gene transfer; viral infection; NS;  
 KW gene; ss.  
 XX OS Influenza A virus.  
 XX PN W02004112831-A2.  
 XX PD 29-DEC-2004.  
 XX PF 27-MAY-2004; 2004WO-US016680.  
 XX PR 28-MAY-2003; 2003US-0473798P.  
 XX PA (WISC ) WISCONSIN ALUMNI RES FOUND.





244	QY	CAGATGAGGCAC	TAAAAATGACCA	TGGCTCTGTTCTCTGCTTCA	CGCTACTTAACTGACA	303
807	Db	CCGATGAGGCAC	TAAAAATGACCA	TGGCTCTGTTCTCTGCTTCA	CGCTACTTAACTGACA	748
304	QY	TGACTCTTGATG	AGATGTCAAGAGA	CTGGTTTCATGCTCATGCCC	CAAGCAAAATAAACAG	363
747	Db	TGACTCTTGAGAG	ATGTCAAGGSA	CTGGTTTCATGCTCATGCCC	CAAGCAAAATAAATGGCAG	688
364	QY	GCTCCCTATGT	ATAGAAATGCA	CAGGCAATCATGGTA	TAGAAACATCATCTTAAAGCAA	423
687	Db	GCTCCCTTTGC	ATCAGAAATGCA	CAGGCAATCATGGTA	TAGAAACATCATCTTAAAGCAA	628
424	QY	ACTTTAGTGTGA	TATTTTCGAAAGG	CTGGAGACACTAAATCTATCT	TAGAGCCTTCAACGAAG	483
627	Db	ACTTCAGTGTGA	TATTTTCGATCG	CTGGAACTCTCATACTATTAAG	GGCTTTTAAACCGATG	568
484	QY	AAGGAGCAGT	CGTTCGGCAAA	TTTTCACCAATTCCTCTTCC	CAGGACATACTAATGAGG	543
567	Db	AGGAGCAAT	TGTCGGGNAAT	TTTTCACCAATTCCTCTTCC	CAGGACATACTGATGAGG	508
544	QY	ATGTCMAAAT	GCANATTTGGGT	CTCATCGGAGGACTTAAATCG	GAATGATTAATACGGTTA	603
507	Db	ATGTCMAAAT	GCANATTTGGGT	CTCATCGGAGGACTTGAATCG	GAATGATTAACACATGTC	448
604	QY	GAATCTCTGAA	ACTTCTACAGAT	TTCGCTTCGAGAGCAGT	CATGAGAACTGGGAGACCTT	663
447	Db	GAATCTCTGAA	ACTTCTACAGAT	TTCGCTTCGAGAGCAGT	TAATGAGATGGGAGCCTC	388
664	QY	CATTCCTCCAA	GCAGAGAAACG	AAATTCGAGAGCAATTTGAG	CCAGCAAGCTTTTGAGAA	723
387	Db	CATTCCTCCAA	GCAGAGAAACG	AAATTCGAGAGCAATTTGAG	CCAGCAAGCTTTTGAGAA	328
724	QY	ATAAGATGTTG	ATTGAAGAGT	CGGACATAGATTGAA	AAATTCAGAAATAGTATTGAA	783
327	Db	ATAAGATGTTG	ATTGAAGAGT	CGGACATAGATTGAG	TAATGAGATTAACAGATATTGAA	268
784	QY	CAAAATAACAT	TTATGCAAGC	TTTACAACATATGCTTGA	GTAGTAAACAGAGATAGAACT	843
267	Db	CAAAATAACAT	TTATGCAAGC	TTTACAACATATGCTTGA	GTAGTAAATGGAGATAGAACT	208
844	QY	TTCTCGTTTC	CAGCTTATTTA	TATGATAAAAAAC	ACCCTTGT	883
207	Db	TTCTCGTTTC	CAGCTTATTTA	TATGATGCGCTAC	GAAAGCTTCT	168

RESULT 9  
AAQ22332  
ID AAQ22332 standard; DNA; 890 BP.  
XX  
AC AAQ22332;  
XX  
DT 14-JUL-1992 (first entry)  
XX  
DE RNA (+), (mRNA) from influenza virus A, synthesised from segment 8.  
XX  
KW Segments 1-8; Ann Arbor H2N2; A; B; C; transcription; ss.  
XX  
OS Influenza A virus.  
XX  
XX WO9203454-A.  
XX  
XX 05-MAR-1992.  
XX  
PF 13-AUG-1991; 91WO-US005742.  
XX  
PR 14-AUG-1990; 90US-00567287.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Cowsett LM, Ecke, Ecker DU;  
XX  
XX WPI; 1992-096817/12.  
XX

Report	Sequence	Score	DB 1	DB 2	Length	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB 379	DB 380	DB 381	DB 382	DB 383	DB 384	DB 385	DB 386	DB 387	DB 388	DB 389	DB 390	DB 391	DB 392	DB 393	DB 394	DB 395	DB 396	DB 397	DB 398	DB 399	DB 400	DB 401	DB 402	DB 403	DB 404	DB 405	DB 406	DB 407	DB 408	DB 409	DB 410	DB 411	DB 412	DB 413	DB 414	DB 415	DB 416	DB 417</
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CC containing the PB2, PB1, PA, NP, and M genes from the A/PuertoRico/8/34  
 CC influenza strain, the NS gene from the A/England/1/53 influenza strain,  
 CC and the HA and NA genes from an influenza virus of interest other than  
 CC A/England/1/53, to obtain a high titer reassortant influenza virus. The  
 CC method is useful for producing a high titer reassortant influenza virus.  
 CC The high titer reassortant influenza viruses are useful for producing  
 CC vaccine compositions. The vaccines are useful for treating or preventing  
 CC influenza viral infections. Genetic engineering techniques allow the  
 CC rapid production of custom made attenuated virus vaccines, but vaccine  
 CC use is limited by the need to use vaccine approved cell lines. The master  
 CC strain A/PuertoRico/8/34 which is the most widely used in producing  
 CC recombinant viruses for vaccine use produces a high titer in MDCK cells,  
 CC which are not certified for use in production of human vaccines, but not  
 CC in vero cells, which are certified for this use. The applicants have  
 CC discovered that replacing the NS gene of the A/PuertoRico/3/24 master  
 CC strain with the NS gene of the A/England/1/53 strain gives reassortant  
 CC virus that produces a high titer in vero cells. This sequence corresponds  
 CC to the coding sequence for the NS1 protein from the A/England/1/53v-a  
 CC influenza strain. This strain encodes the protein with the amino acid  
 CC changes Q21R/T58I/V60A/N127S/V174I/D189N/delta231-238.  
 CC  
 XX Sequence 824 BP; 263 A; 167 C; 203 G; 191 T; 0 U; 0 Other;

Query Match 78.0%; Score 692.8; DB 14; Length 824;  
 Best Local Similarity 90.0%; Pred. No. 5.9e-184;  
 Matches 742; Conservative 0; Mismatches 82; Indels 0; Gaps 0;  
 OY 22 ACATATGATTCGACCACTGTGTCAAGCTTTCAGGTAGACTGTCTTTCTTTGGCATGTCC 81  
 DB 1 ACATATGATTCGACCACTGTGTCAAGCTTTCAGGTAGACTGTCTTTCTTTGGCATGTCC 60  
 OY 82 GCAACGATTTGCGAGCAAGAACTCGGGTGATGCCCATTCCTTTGACCGGCTTCGCCGAG 141  
 DB 61 GCAACGATTTGCGAGCAAGAACTAGGTGATGCCCATTCCTTTGATCGGCTTCGCCGAG 120  
 OY 142 ACCAGAAATCCCTAAAGGAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTC 201  
 DB 121 ATCAGAAATCCCTAAAGGAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTC 180  
 OY 202 GTCGAGGAAGCAGATGTGGACAGATTCGGAGAGGATCAGATGAGCAGCTTAAATA 261  
 DB 181 GTCTGGAAGCAATATGTGGCGGATTCGAGAGAGATTCGATGAGGACCTTAAATA 240  
 OY 262 TGACATTCGCTTGTCTTCTGCTTCAAGCTTAACTGATGATGATGATGATGATGATGATG 321  
 DB 241 TGACATTCGCTTGTCTTCTGCTTCAAGCTTAACTGATGATGATGATGATGATGATGATG 300  
 OY 322 CAAGAGACTGGTTCATGCTCATGCCCAAGCAAGAACTACAGGCTCCCTATGTATGAAGA 381  
 DB 301 CAAGAGACTGGTTCATGCTCATGCCCAAGCAAGAACTAGGAGGCTCCCTTGTATCAGA 360  
 OY 382 TGACACGAGCAATCATGTATAAGAACTATCATCTTAAAGCAAACTTTTACTGTGATTTTCG 441  
 DB 361 TGACACGAGCAATCATGTATAAGCAATCATCTTAAAGCAAACTTTTACTGTGATTTTG 420  
 OY 442 AAAGCTGAGGACATTAATCTACTTACTAGGCTTCAAGGAGAGAGAGAGAGAGAGAGAGAG 501  
 DB 421 ACCGCTGAGGACATTAATCTACTTACTAGGCTTCAAGGAGAGAGAGAGAGAGAGAGAGAG 480  
 OY 502 AAATTTACCAATTCGCTTCTTCTCCAGGACATCATTAATGAGGATGTCAAAATGCAATTG 561  
 DB 481 AAATTTACCAATTCGCTTCTTCTCCAGGACATCATTAATGAGGATGTCAAAATGCAATTG 540  
 OY 562 GGGTCTCTCATCGGAGGACTTAAATGGAATGATAATACGGTTAGAACTCTCTGAAACTCTAC 621  
 DB 541 GGGTCTCTCATCGGAGGACTTAAATGGAATGATAATACGGTTAGAACTCTCTGAAACTCTAC 600  
 OY 622 AGAGATTCGCTTGGAGAGAGAGATCATGAGATGGGAGAGCTTCATTCCTTCCCAAGAGAG 681  
 DB 601 AGAGATTCGCTTGGAGAGAGAGATCATGAGATGGGAGAGCTTCATTCCTTCCCAAGAGAG 660  
 OY 682 AACGAATGAGAGAGAGAGATTCAGGAGAGAGATTCAGAAATAGATGATGATGATGATGATG 741

DB 661 AACGAAAATGCGGAGAACAAATTAGCTCAGAAAGTTTGAAGAAATAGATGTTGATGAA 720  
 OY 742 GAAGTGCATAGATTCGAAATATACAGAAATAGTTTGAACAAATAGATGTTGATGAA 801  
 DB 721 GAAGTGCATAGATTCGAAATATACAGAAATAGTTTGAACAAATAGATGTTGATGAA 780  
 OY 802 GCCTTCAACTATTCCTTGAAGTACAGAGAGATGATGATGATGATGATGATGATGATGAT 845  
 DB 781 GCCTTCAACTATTCCTTGAAGTACAGAGAGATGATGATGATGATGATGATGATGATGAT 824

RESULT 13  
 AAT37435  
 ID AAT37435 standard; DNA; 693 BP.  
 XX AAT37435;  
 XX AC  
 XX 16-OCT-2003 (revised)  
 DT 09-APR-1997 (first entry)  
 XX  
 XX Non-structural protein NS1 of influenza A virus.  
 XX  
 XX Non-structural protein; NS1; influenza virus; respiratory tract;  
 KW diagnosis; anti-NS1 antibody; primer; PCR; detection; amplify; ss.  
 XX  
 XX Influenza virus; A/equine 1/Suffolk 89.  
 XX  
 XX BP726316-A2.  
 XX  
 XX 14-AUG-1996.  
 XX  
 XX 31-JAN-1996; 96BP-00300681.  
 XX  
 XX 09-FEB-1995; 95GB-00002489.  
 XX  
 XX (ANIM-) ANIMAL HEALTH TRUST.  
 XX  
 XX Binns M, Birch-Machin I;  
 XX  
 XX WPI: 1996-364394/37.  
 DR P-PSDB; AAW03522.  
 XX  
 PT Recombinant equine influenza virus NS1 protein - useful for diagnosis of  
 PT equine influenza A.  
 XX  
 PS Claim 1; Fig 1A; 20pp; English.  
 XX  
 CC This sequence encodes non-structural protein NS1 of influenza virus  
 CC A/equine 2/Suffolk 89. The NS1 protein is useful for diagnosis of equine  
 CC influenza A infections by detection of anti-NS1 antibodies. The NS1  
 CC coding sequence was isolated using the primer sequences given in AAT37436  
 CC -40. (Updated on 16-OCT-2003 to standardise OS field)  
 XX  
 XX Sequence 693 BP; 215 A; 146 C; 166 G; 166 T; 0 U; 0 Other;

Query Match 77.1%; Score 685; DB 2; Length 693;  
 Best Local Similarity 99.3%; Pred. No. 8.5e-182;  
 Matches 688; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 OY 27 ATGGATTCACCACTGTGTCAAGCTTTCAGGTAGACTGTCTTTCTTTGGCATGTCCGAAA 86  
 DB 1 ATGGATTCACCACTGTGTCAAGCTTTCAGGTAGACTGTCTTTCTTTGGCATGTCCGAAA 60  
 OY 87 CGATTTGCGAGACCAAGAACTGGGTGATGCCCATTCCTTACCGGCTTGGCCGAGACGAG 146  
 DB 61 CGATTTGCGAGACCAAGAACTGGGTGATGCCCATTCCTTACCGGCTTGGCCGAGACGAG 120  
 OY 147 AAGTCCCTTAAAGGAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGA 206  
 DB 121 AAGTCCCTTAAAGGAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGA 180  
 OY 207 GGAAAGCAGATGTGGAGCAGATTCCTGGAGAGAGATTCAGATGAGGACTTAAATGACC 266

Db 181 GGAAGACAGATAGTGGAGCAGATTTCTGGAAGAGATCAGATGAGGCATTTAAATGACC 240  
Qy 267 ATGCTCTGTCTGCTTCCGCTTACGCTTACTTAATCACTGATCACTCTTGATGAGATGTCAGA 326  
Db 241 ATGCTCTGTCTGCTTCCGCTTACTTACTGATGATGATGATGATGATGATGATGATGATGAT 300  
Qy 327 GACTGGTTCATGCTCATGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 386  
Db 301 GACTGGTTCATGCTCATGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
Qy 387 CAGGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 446  
Db 361 CAGGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
Qy 447 CTGGAGACACTAATCTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 506  
Db 421 CTGGAGACACTAATCTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 480  
Qy 507 TCACCAATTCCTTCTCTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGCTC 566  
Db 481 TCACCAATTCCTTCTCTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGCTC 540  
Qy 567 CTCATCGAGGACTTAAATGGAATGATATACGGTTAGAACTCTGAACTCTACAGAGA 626  
Db 541 CTCATCGAGGACTTAAATGGAATGATATACGGTTAGAACTCTGAACTCTACAGAGA 600  
Qy 627 TTCGCTTGGAGAGCAGTCATGAGAAATGGAGACCTTCATTCCTCCAAAGCAGAAACGA 686  
Db 601 TTCGCTTGGAGAGCAGTCATGAGAAATGGAGACCTTCATTCCTCCAAAGCAGAAACGA 660  
Qy 687 AATATGGAGAACAAATGAGCCAGAGAGTTTGA 719  
Db 661 AATATGGAGAACAAATGAGTCAGAGTTTGA 693

RESULT 14  
ID ADY62117 standard; DNA; 824 BP.  
AC ADY62117;  
XX  
XX 19-MAY-2005 (first entry)  
XX Influenza A virus strain A/England/1/53 wild type NS1 gene for vaccine.  
XX protein engineering; immune stimulation; immunostimulant; vaccine;  
XX Influenza virus infection; gene; ds.  
XX Influenza A virus; strain A/England/1/53.  
XX Key Location/Qualifiers  
XX CDS 6..719  
XX /\*tag= a  
XX /product= "Influenza A virus NS1 protein"  
XX /note= "no stop codon given"  
XX US2005054846-A1.  
XX 10-MAR-2005.  
XX 04-SEP-2003; 2003US-00654737.  
XX 04-SEP-2003; 2003US-00654737.  
XX (WEBS/) WEBSTER R G.  
XX (WEBB/) WEBBY R J.  
XX (OZAK/) OZAKI H.  
XX Webster RG, Webby RJ, Ozaki H;  
XX WPI; 2005-213104/22.  
XX P-PSDB; ADY62119.

PT Producing a reassortant influenza virus that gives a high titer in Vero  
PT cells (certified for use in vaccine-production), comprises replacing the  
PT NS gene of the A/PuertoRico/3/24 master strain with the NS gene of the  
PT A/England/1/53 strain.  
PS Claim 7; SEQ ID NO 1; 16pp; English.  
XX The invention relates to a method of producing a high titer reassortant  
XX influenza virus by transfecting host cells with expression plasmids  
XX containing the PB2, PB1, PA, NP, and M genes from the A/PuertoRico/8/34  
XX influenza strain, the NS gene from the A/England/1/53 influenza strain,  
XX and the HA and NA genes from an influenza virus of interest other than  
XX A/England/1/53, to obtain a high titer reassortant influenza virus. The  
XX method is useful for producing a high titer reassortant influenza virus.  
XX The high titer reassortant influenza viruses are useful for producing  
XX vaccine compositions. The vaccines are useful for treating or preventing  
XX influenza viral infections. Genetic engineering techniques allow the  
XX rapid production of custom made attenuated virus vaccines, but vaccine  
XX use is limited by the need to use vaccine approved cell lines. The master  
XX strain A/PuertoRico/8/34 which is the most widely used in MDCK cells,  
XX recombinant viruses for vaccine use produces a high titer in MDCK cells,  
XX which are not certified for use in production of human vaccines, but not  
XX in Vero cells, which are certified for this use. The applicants have  
XX discovered that replacing the NS gene of the A/PuertoRico/3/24 master  
XX strain with the NS gene of the A/England/1/53 strain gives reassortant  
XX viruses that produces a high titer in Vero cells. This sequence corresponds  
XX to the coding sequence for the NS1 protein from the A/England/1/53  
XX influenza strain.

Sequence 824 BP; 267 A; 167 C; 201 G; 189 T; 0 U; 0 Other;  
Query Match 77.1%; Score 684.8; DB 14; Length 824;  
Best Local Similarity 89.4%; Pred. No. 1e-181;  
Matches 737; Conservative 0; Mismatches 87; Indels 0; Gaps 0;  
Qy 22 ACATATGATTCGACACACTGCTCAGCTTTTCAGTGTAGTCTTTTTCGTCATGTCC 81  
Db 1 ACATATGATTCGACACACTGCTCAGCTTTTCAGTGTAGTCTTTTTCGTCATGTCC 60  
Qy 82 GCAAAACGATTTGACAGACCAAGAACTGGGTGATGCCCATCTCTTGACGGCTTCGCCGAG 141  
Db 61 GCAAAACGATTTGACAGACCAAGAACTGGGTGATGCCCATCTCTTGATCGGCTTCGCCGAG 120  
Qy 142 ACCAAGAGTCCCTTAAAGAGAGGTAGTACCTCTTGGTCTGCATCGAATCGAACAGCCACTC 201  
Db 121 ATCAGAAAGTCCCTTAAAGAGAGGTAGTACCTCTTGGTCTGCATCGAATCGAACAGCCACTC 180  
Qy 202 GTGCAGGAAAGCAGATAGTGGAGCAGATCTCTGGAAGAGGATCAGATGAGGCATTTAAAA 261  
Db 181 GTGTGGAAGAGCAGATAGTGGAGCAGATCTCTGGAAGAGGATCAGATGAGGCATTTAAAA 240  
Qy 262 TCACCATTCGCTCTGTTCTGCTTCACTGCTTCACTTACTGATGATGATGATGATGATGATGAT 321  
Db 241 TCACCATTCGCTCTGTTCTGCTTCACTGCTTCACTTACTGATGATGATGATGATGATGATGAT 300  
Qy 322 CAAGAGACTGTTTCATGCTCATGCTCCAGCAGAAAGTAAACAGGCTCCCTATGATGATGAT 381  
Db 301 CAAGGGAAGTCTGTTTCATGCTCATGCTCCAGCAGAAAGTAAACAGGCTCCCTATGATGATGAT 360  
Qy 382 TGGACACGAGCAATCATGGATAAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTCG 441  
Db 361 TGGACACGAGCAATCATGGATAAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTCG 420  
Qy 442 AAAGGCTGAGACACTAAATCTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 501  
Db 421 ACCGGCTGAGACACTAAATCTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 480  
Qy 502 AAATTTTCAACATTCCTCTTCTTCCAGGACATCTAATAGGATGATGATGATGATGATGATGAT 561  
Db 481 AAATTTTCAACATTCCTCTTCTTCCAGGACATCTAATAGGATGATGATGATGATGATGATGAT 540  
Qy 562 GGGTCTCTCATCGAGGAGCTTAAATGGAATGATGATGATGATGATGATGATGATGATGATGAT 621

Db 541 GGGTCTCATCGGAGACTTGAATGAATGATTAACACAGTTCGAGTCTCTAAACTCTAC 600  
 Qy 622 AGAGATTTCGCTTGAGAGAGCAGTCAATGAGATGGAGACCTTCATTCCCTCCAAAGCAGA 681  
 Db 601 AGAGATTTCGCTTGAGAGAGCAGTCAATGAGATGGAGACCTTCACCTCACTCCAAACAGA 660  
 Qy 682 AACGAAATCGAGAGAACAAATTTGAGCCAGAGTTCGAAGAAATAGATGGTTCATTGAA 741  
 Db 661 AACGAAATCGAGAGAACAAATTTAGTCTCAGAGTTCGAAGAAATAGATGGTTCATTGAA 720  
 Qy 742 GAAGTGCACATACATTAAGAAATACGAAATAGTTCGAACAAATACATTTATCGAA 801  
 Db 721 GAAGTGCACACAAATTTGAGATTAACAGAGATAGTTCGACAAATACATTTATCGAA 780  
 Qy 802 GCTTACAACTATTGCTTGAAGTGAACAGAGATAGACCTTT 845  
 Db 781 GCTTACAGTACTGTTTGAAGTGAACAGAGATAGACCTTT 824

## RESULT 15

AAID15680  
 ID AAD15680 standard; DNA; 468 BP.

XX AC AAD15680;

XX DT 15-NOV-2001 (first entry)

XX DE Equine influenza virus H3N8 neiwt4NS468 DNA.

XX KW Equine influenza virus; ei; cold adaptation; temperature sensitivity;  
 KW vaccine; neiwt4NS468 DNA; Peiwt4NS97 protein; ds.

XX OS Equine influenza virus H3N8.

PH Key Location/Qualifiers

FT misc\_feature 1..293

FT /tag= b

FT /note= "this region is specifically claimed as SEQ ID NO:  
 38 in claim 2 of the specification"

FT CDS 3..296

FT /tag= a "Peiwt4NS97 protein /note "CDS does not include  
 start codon"

FT /partial

XX WO200160849-A2.

XX PN 23-AUG-2001.

XX PD 16-FEB-2001; 2001WO-US005048.

XX PF 16-FEB-2000; 2000US-00506286.

XX PR (UYPI-) UNIV PITTSBURGH.

XX PA DOWLING PW, Youngner JS;

XX PI WPI; 2001-522584/57.

XX DR P-PSDB; AAE09028.

XX PT Novel isolated equine influenza virus (wild-type and cold-adapted)

XX PT proteins and viruses containing nucleic acid molecules encoding the

XX PT proteins, which are useful for protecting animals from influenza virus

XX PT infections.

XX PS Claim 2; Page 74-75; 172pp; English.

XX CC The patent discloses cold-adapted equine influenza viruses and

XX CC reassortant influenza A viruses comprising at least one genome segment of

XX CC such an equine influenza virus, wherein the equine influenza virus genome

XX CC segment confers at least one identifying phenotype of the cold-adapted

XX CC equine influenza virus, such as cold adaptation, temperature sensitivity,

XX CC dominant interference or attenuation. The viruses are useful for

CC protecting animals from diseases caused by influenza viruses. They are  
 CC also used as vaccines. The present sequence is equine influenza (ei)  
 CC virus H3N8 neiwt4 (wild type) NS468 DNA encoding Peiwt4NS97 protein  
 XX  
 SQ Sequence 468 BP; 168 A; 80 C; 98 G; 122 T; 0 U; 0 Other;

Query Match 52.2%; Score 463.4; DB 4; Length 468;

Best Local Similarity 99.8%; Pred. No. 1.3e-119;

Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 424 ACTTATGCTGATTTTTCGAAGGCTGGAGACACTAATACTACTACTACGCTTCACCGAG 483  
 Db 1 ACTTATGCTGATTTTTCGAAGGCTGGAGACACTAATACTACTACTACGCTTCACCGAG 60  
 Qy 484 AAGGACAGTCTGCTGGGAAATTTTCAACATTCCTTCTCTCCAGGACATACATGAGG 543  
 Db 61 AAGGACAGTCTGCTGGGAAATTTTCAACATTCCTTCTCTCCAGGACATACATGAGG 120  
 Qy 544 ATGTCAAAATGCAATTTGGGCTCTCATCGAGGACTTAAATGGAATGATACGGTTA 603  
 Db 121 ATGTCAAAATGCAATTTGGGCTCTCATCGAGGACTTAAATGGAATGATACGGTTA 180  
 Qy 604 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGAATGGAGACCTT 663  
 Db 181 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGAATGGAGACCTT 240  
 Qy 664 CATTCCCTCCAAAGCAGAAACGAAATGGAGAGAACAAATTTGAGCCAGAGTTTGAAGAA 723  
 Db 241 CATTCCCTCCAAAGCAGAAACGAAATGGAGAGAACAAATTTGAGCCAGAGTTTGAAGAA 300  
 Qy 724 ATAAGATGCTTGAATGGAAGTCCGACATAGATTGAAAATACAGAAAATAGTTTTCGA 783  
 Db 301 ATAAGATGCTTGAATGGAAGTCCGACATAGATTGAAAATACAGAAAATAGTTTTCGA 360  
 Qy 784 CAAATAACATTTATGCAAGCTTACAACTATTGCTTGAAGTAGAACAGAGATAAGAACT 843  
 Db 361 CAAATAACATTTATGCAAGCTTACAACTATTGCTTGAAGTAGAACAGAGATAAGAACT 420  
 Qy 844 TTCTCGTTTCAGCTTATTTAATGATAAATAACACCCCTTGTTCTTA 888  
 Db 421 TTCTCGTTTCAGCTTATTTAATGATAAATAACACCCCTTGTTCTTA 465

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 Job time : 561.673 secs

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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 00:06:39 ; Search time 4487.83 Seconds  
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Title: US-10-734-373-57

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_hic.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_est7.\*  
9: gb\_gsa1.\*  
10: gb\_gsa2.\*  
11: gb\_gsa3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59.4	6.7	1101	10	CNS0039G
2	55.2	6.2	1101	10	CNS0006J
3	54.8	6.2	899	11	CNS03X3Y
4	48.6	5.5	929	11	CNS07BEP
5	47.2	5.3	1164	10	CL035484
6	47.2	5.3	1227	7	CK210809
7	47	5.3	1101	10	CNS0039R
8	46.4	5.2	576	9	CE229067
9	46.4	5.2	1268	10	AG311044
10	46.2	5.2	675	9	BH988095
11	46.2	5.2	759	11	CNS060XV
12	46.2	5.2	857	9	AZ688092
13	46.2	5.2	1316	10	AG304883
14	46.2	5.2	2565	4	AK020016
15	45.6	5.1	1514	10	AG311217
16	45.4	5.1	521	9	BH71630
17	45.4	5.1	701	9	BH711431
18	45.2	5.1	408	10	CNS00983
19	45.2	5.1	645	3	BM167957
20	45.2	5.1	947	10	CW951010
21	45.2	5.1	1213	10	AG277918
22	45	5.1	718	9	BZ510433

C 23	44.8	5.0	838	9	AZ138945
C 24	44.8	5.0	1278	10	AG278227
C 25	44.6	5.0	857	10	CNS01831
C 26	44.6	5.0	2017	4	AK090268
C 27	44.4	5.0	687	9	BH723944
C 28	44.4	5.0	760	9	BZ461276
C 29	44.4	5.0	1116	10	CL116360
C 30	44.4	5.0	1201	10	CNS018FX
C 31	44.2	5.0	823	10	CW953861
C 32	44.2	5.0	859	10	CZ998571
C 33	44.2	5.0	899	10	CW947334
C 34	44	5.0	509	3	BM952076
C 35	44	5.0	665	2	BG854775
C 36	44	5.0	666	9	CC964328
C 37	44	5.0	704	9	BH941436
C 38	44	5.0	705	9	BH485727
C 39	43.8	4.9	618	9	BH657329
C 40	43.8	4.9	631	10	CNS02NKC
C 41	43.8	4.9	964	11	CNS07B8R
C 42	43.6	4.9	375	10	CE364194
C 43	43.6	4.9	1129	10	AG305138
C 44	43.6	4.9	1203	10	AG377060
C 45	43.4	4.9	443	3	BM170766

## ALIGNMENTS

RESULT 1  
CNS0039G/c

LOCUS 1101 bp DNA linear GSS 03-JUN-1999  
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
ACCESSION AL063921  
VERSION AL063921.1 GI:4941778  
KEYWORDS GSS.  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE Direct Submission  
AUTHORS Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
TITLE BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
JOURNAL - Web : www.genoscope.cns.fr)

COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oosagawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
Location/Qualifiers  
1..1101

/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR08K10"  
/clone\_lib="RPCI-98"  
/note="end : TET3"

ORIGIN

Wed Mar 8 09:11:19 2006

Query Match 6.7%; Score 59.4; DB 10; Length 1101;  
Best Local Similarity 14.7%; Pred. No. 8e-05;  
Matches 76; Conservative 242; Mismatches 199; Indels 0; Gaps 0;

QY 372 TGTATGAAGTGGACGACCAATCATGATGAAGACATCATCTATTAAGCAACTTACT 431  
DB 1071 DRADRDWAGDADWDGAGTGTATWWWWWWATWTWTDKWWWWATAKTDTWT 1012  
QY 432 GTGATTTTCGAAAGGCTGGAGACACTAATCTAGTCTAGAGCCCTCCAGCAAGAGCA 491  
DB 1011 WRTAWRADWAGRGAGKEDDAATDAGAGRRDGRKDKDKDKDDDKKGGKK 952  
QY 492 GTGCTGGCGAAATTCACCATTCCTCTCCAGGACATCACTAATGAGGATCTCAA 551  
DB 951 AAKAAKATATKWWDDWDKWDGAKDKKADDDGAGKDDGDKDDDTGDKDD 892  
QY 552 AATGCAATTTGGGGTCTCATCGGAGGACTTAAATGGAATGATATACGGTGAATCTCT 611  
DB 891 DKDKDDWDKAKGTGWDATWAAATDWWMGWADADWTTWDAADDDWADRDWDAWKW 832  
QY 612 GAACTCTACAGATTCGCTTCGAGAGCAGTCATGAGAAATGGGAGACCTTCATCTCT 671  
DB 831 DDAAWAGARTADRDWDGDRAGKRGARKERDRKADDDKDDADDDAATTTTTR 772  
QY 672 CCAAGCAGAAACGAAATCGAGAGCAATTCGAGCAGAGTTCGAGAAATAAGATG 731  
DB 771 DTDKWKTDWTRWAADRTWDRDDDDDRDAGTAGRKRRTWKREKRDTRWDDAD 712  
QY 732 GTTGATTGAAGAGTGCACATAGATTGAAATAATACAGAAATAGTTTGAACAATAAC 791  
DB 711 DTAARDRRRGDGDAGKGTGRKRRDRATWDRTDWADADAAMWTTTDTDDWDK 652  
QY 792 ATTATGACGCTTACCACTATTGCTGAGTACAGAGATAGAACTTTCTCTGTT 851  
DB 651 RDRRKGARRRTTARAADWWTWKAWDKWTKTRADRDWRWAADTTWTDKADRW 592  
QY 852 TCAGCTATTATGATTAATAAAACACACCTTTGTTCTA 888  
DB 591 AKARWARRDRARARADRETTTGGTTTATTTWA 555

RESULT 2  
CNS0006J 1101 bp DNA linear GSS 03-JUN-1999  
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #  
DEFINITION BACR01M22 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL062049.1 GI:4938511  
VERSION AL062049.1  
KEYWORDS GSS.  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 1101)  
Genoscope.  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr)  
- Web : www.genoscope.cns.fr  
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ogasawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).  
Location/Qualifiers  
1. 1101  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR01M22"  
/clone\_lib="RPCI-98"  
/note="end : TET3"

ORIGIN  
Query Match 6.2%; Score 55.2; DB 10; Length 1101;  
Best Local Similarity 23.8%; Pred. No. 0.0011;  
Matches 80; Conservative 116; Mismatches 140; Indels 0; Gaps 0;

QY 541 AGGATCTCAAAAATGCAATTTGGGGTCTCATCGGAGGACTTAAATGGAATGATATACGG 600  
DB 721 RGGGGGRAWRAAAAATKTKKKTKTKRKAAGRRBARAWAGAAAAAADAADATKTGK 780  
QY 601 TTGAATCTCTGAAATCTTACAGAGATTCGCTTCGAGAGCAGTCATGAGAAATGGGAGAC 660  
DB 781 TWAKAARWTAWKDKWKATDAAAATAAARTRDWTAKAKDKTKWGAATAATGAWGAGAARG 840  
QY 661 CTTCTATTCCTCCAAAGCAGAAACGAAATTCGAGAGCAACAATTCGAGCCAGAGATTGAA 720  
DB 841 RWRGKGDGTREAREAGGAGDGDWAKAWAWAAWAATTAADDDRAKADWKA 900  
QY 721 GAATAGATGCTGTGATTGAAGAAGTGCACATAGATTGAAATAATACAGAAATAGTTT 780  
DB 901 AAADRDKDKGRAGGTGWRERRARTRKAKRKGARAGAKAKRRAKADWADKDKK 960  
QY 781 GAACAATACCAATTTTCAAGCTTACCACTATTGCTTGAAGTAGAACAAGAGATAAGA 840  
DB 961 WDKDAWAKAKGTGDWKKRARKTKGWARADKDRWRAAADTRWTKAWMTDWRWAT 1020  
QY 841 ACTTCTCTGCTTCAGCTTATTATGATATAAAACA 876  
DB 1021 ATKDKTKAKKAGKANKTTTIDRAKAKAKDDTA 1056

RESULT 3  
CNS03X3Y 899 bp DNA linear GSS 01-SEP-2000  
LOCUS Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone  
DEFINITION 065807 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL264535  
VERSION AL264535.1 GI:7986236  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetraodon nigroviridis  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraontoidea; Tetraodontidae; Tetraodon.  
1  
Roest Crolius.H., Jallou.O., Dasilva.C., Bouneau.L., Fisher.C., Bernot.A., Fizames.C., Wincker.P., Brottier.P., Quetier.F., Saurin.W. and Weissenbach.J.  
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
Nat. Genet. 25 (2), 235-238 (2000)  
10835645  
2  
Roest Crolius.H., Jallou.O., Dasilva.C., Ozouf-Costaz.C., Fizames.C., Fischer.C., Bouneau.L., Billault.A., Quetier.F., Saurin.W., Bernot.A. and Weissenbach.J.  
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
Genome Res. 10 (7), 939-949 (2000)  
10899143  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED



ORGANISM Xenopus tropicalis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
Xenopodinae; Xenopus; Silurana.

REFERENCE 1 (bases 1 to 1164)  
AUTHORS Krenitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,  
Mardis, E. and Wilson, R.

TITLE A physical map of the xenopus tropicalis genome  
JOURNAL Unpublished (2003)  
COMMENT Contact: Richard K Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@wustl.edu  
Insert Length: 175000 Std Error: 0.00  
Seq primer: Sp6 ATTAGGTGACACTATAG  
Class: BAC ends  
High quality sequence start: 18  
High quality sequence stop: 284.

FEATURES  
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1..1164  
Location/Qualifiers  
/organism="Xenopus tropicalis"  
/mol\_type="genomic DNA"  
/strain="Nigerian frog"  
/db\_xref="taxon:8364"  
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/sex="male"  
/cell\_line="Stock 248 F7A2, inbred N7"  
/clone\_lib="CH216"  
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis  
BAC library"

ORIGIN  
Query Match 5.3%; Score 47.2; DB 10; Length 1164;  
Best Local Similarity 52.0%; Pred. No. 0.18;  
Matches 106; Conservative 0; Mismatches 98; Indels 0; Gaps 0;  
QY 675 AACGAGAGAGAAATCGAGAGACAAATTCAGCCAGAGATTTGAAGAAATAGATGTT 734  
Db 558 AAGATATAGTATATATTAATGAAGATGATATACGAAATAGAGATAGTATAAATAA 499  
QY 735 GATTGAGAGTGCACATAGATTGAAGAAATACAGAAATAGTTTGAACAATAACATT 794  
Db 438 TAGTCAGAGAGAAATAAATGTTGMAAAATAAAGAAAATTAATAAATATTTTTTTT 439  
QY 795 TATCGAGCTTACACTATTGCTTGAAGTAGAACAAGAGATAGAACTTTCTCGTTTCA 854  
Db 438 TAAAGAGCGATTAGTATTGGGGGGGAGAGAAAAGAAAATATAATTTAGTATGC 379  
QY 855 GCTTATTATGATATAAAACACC 878  
Db 378 AAGGATATATGATATAACAC 355

RESULT 6  
CK210809 1227 bp mRNA linear EST 08-DEC-2003  
LOCUS FGAS022636 Triticum aestivum FGAS: Library 5 GATE 7 Triticum  
DEFINITION aestivum cDNA, mRNA sequence.  
CK210809.1 GI:39573199  
Triticum aestivum (bread wheat)  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 1227)  
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,  
Genswein, B., Graf, R., Gulik, P., Hrycan, L.D., Larocque, A.,  
Links, M.G., McCarthy, E.L., McNamara, J., Muzak, I., Nilsson, D.,  
Penniket, C., Roach, J.D. and Sarhan, F.  
Functional Genomics of Abiotic Stress in Wheat and Canola Crops  
Unpublished (2003)

COMMENT Contact: Wm L Crosby  
Bioinformatics  
University of Saskatchewan, Department of Computer Science  
1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
Saskatchewan, S7N 5A9, Canada  
Tel: 306 966 1769  
Fax: 306 966 2033  
Email: fgas\_est@cs.usask.ca  
This sequence is the direct result of the Base calling software  
Phred (default parameters). It is the raw base calls. To aid in the  
identification of the high quality insert the software Lucy  
(default parameters) has been run on this sequence. Lucy identified  
the region [44..369].  
Plate: L5B024 row: A column: 08.

FEATURES  
source  
1..1227  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:4565"  
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/note="Vector: PCMV.SPORT6; Crown and developmental stages  
of spike formation in wheat cultivar Norstar. 4 mRNA  
Populations were combined before constructing the library.  
The first mRNA population is from lcm crown sections after  
30 days of cold acclimation. The second is from lcm crown  
sections after 11 days of deacclimation (before  
deacclimation plants were fully vernalized for 49 days).  
The third is from different developmental stages of spike  
formation (5 to 50mm) that still have not emerged from the  
leaf (dissection required). The last is from different  
developmental stages of spike and seed formation after  
having emerged from the leaf (visible). First strand  
synthesis in this library was done in the presence of  
methylated dCTP thereby protecting from internal cleavage  
with NotI."

ORIGIN  
Query Match 5.3%; Score 47.2; DB 7; Length 1227;  
Best Local Similarity 47.6%; Pred. No. 0.19;  
Matches 100; Conservative 0; Mismatches 110; Indels 0; Gaps 0;  
QY 632 TTGCGAGACGCTCATGAGATGGAGACCTTCATTCCTCCCAAGCAGAAACGAAAAAT 691  
Db 601 TTGCGGGGGCGCTGTAAANAACAAGCGCTTCNATCCCGCTTCNNNNNNAAAAA 660  
QY 692 GGAGAGAACAAATGAGCCAGAGATTTCGAAGAATAAGATGTTGATTGAAGAAGTCGCAC 751  
Db 661 GANPAANCAAN 720  
QY 752 ATAGATTGAATAATCAGAAATAGTTTTCGAACAATAACATTTATGCAAGCTTACAAC 811  
Db 721 GAATAATCAAN 780  
QY 812 TATTCCTTGAAGTAGACAGAGATAGAA 841  
Db 781 AATTATATATAAAGATCAANANANANANANANANANANANANANANANANAN 810

RESULT 7  
CNS0039R 1101 bp DNA linear GSS 03-JUN-1999  
LOCUS Drosohila melanogaster Genome survey sequence TET3 end of BAC #  
DEFINITION BACH08010 of RPCL-98 library from Drosohila melanogaster (fruit  
fly), genomic survey sequence.  
AL063932.1 GI:4941789  
Drosohila melanogaster (fruit fly)  
Drosohila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosohiliidae; Drosohila.  
1 (bases 1 to 1101)





library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
Tsukuba Institute, Bio Resource Center,  
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyadi, Tsukuba, 305-0074 Japan  
Phone: 81-298-36-9189, fax: 81-298-36-9199  
E-mail: abe@rtc.riken.jp  
PRIMRES

```

Sequencing : T7
LIBRARY
Vector      : pBACE3.6
R_Site 1   : EcoRI
R_Site 2   : EcoRI.

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```

Location/Qualifiers
1. .1268
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMG01-093K15.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMG01 Mouse Male BAC Library"

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	5.2%; Similarity 92; Conservative	Score 46.4%; Pred. No. 0.31; 0; Mismatches	DB 10; Length 1268; Indels 76;	Gaps 0;
74	AAACGAGAACGAAAAATCGAGGAGACAAATTGAGCCGAGAGTTTGAAGAAATAAGATGCT	733		
14	AAAGAGGAGAGATGAAGATTAATGAGTAAATAAGACAAAGGGAAGACGAAGAAGATAGA	855		
34	TCATTTGAAGAAAGTCGCGCATAGATTGTAAAAATACAGAAATAGTTTTCGACAAATAACAT	793		
54	TGGAAGGGAAGAGGAGAAAAAGAAAAAGAAAAAGGGGAAAAATAGNGATAGAGNATTAAGAA	795		
94	TTATCGAAGCCCTTAACTATTCTTTGAAGTAGAACGAAGATAGA	841		
94	AGAGAGAGATGTAAAAAAAAGAAAAAGATGATGAAGAAAAAGAAAGCGGTGAGAA	747		

BH988095 675 bp DNA linear GSS 07-OCT-2000  
ocj5a02.b1 *B. oleracea*002 *Brassica oleracea* genomic, genomic survey  
sequence.  
BH988095  
BH988095.1 GI:23523848  
GSS.  
*Brassica oleracea*  
*Brassica oleracea*  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 675)  
Delehaanty,K., Fwell,G., Fulton,L., McCombie,W.R., Miner,T.,  
Nash,W., Rabinowicz,P.D. and Wilson,R.K.  
Whole genome shotgun reads from *Brassica oleracea*

Unpublished (2002)  
Contact: Richard K. Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@watson.wustl.edu  
Plate: cej25 row: a column: 02  
Seq primer: -21UpOT forward  
Class: shotgun  
High quality sequence start: 95  
High quality sequence stop: 551.  
Location/Qualifiers  
1. .675  
/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3712"

/clone.lib=FB.cleracea002" Whole genome shotgun library from notes=vector.F0W13; The whole genome shotgun library from following buds DNA was purified from a crude nuclear prep using Basic Clereaca TO1000DH buds provided by Dr. Thomas O'Brien at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHU) and the whole genome shotgun library prepared at Washington University Genome Sequencing Center."

Query Match	5.2%;	Score 46.2;	DB 9;	Length 675;
Best Local Similarity	53.6%;	Pred. No. 0.3;		
Matches 96;	Conservative	0;	Mismatches 83;	Indels 0;
Gaps				
687	AAATGCGAGAGACAATGCGGCCGACAGCTTTGAGCAAAATAGATGCTTCATTGAAGAAGT	746		
693				
694				
695				
696				
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787				
788				
789				
790				

RESULT 11				GSS 05-JUL-2001
CNS06QXV			759 bp	DNA linear
CNS06QXV			T7 end of clone AWAAA009H09	of library AW0AA from strain CLIB 89 of
LOCUS				<i>varroa lipolytica</i> , genomic survey sequence.
DEFINITION				

Accession	Version	GI	Organism
AL411257			<i>Yarrowia lipolytica</i>
AL411257.1		GI:12180512	<i>Yarrowia lipolytica</i>
GSS			Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Dipodaseaceae; <i>Yarrowia</i> .
1			(bases 1 to 759)

NUMBER	AUTHORS	TITLE	JOURNAL
1	Souciet J.L., Aigle, M., Artiguenave, P., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casareggi, S., de Montigny, J., Dujon, B., Durans, P., Lepingle, A., Llorente, P., Maupertuy, A., Neuvéglise, C., Olsier-Kalogirakou, O., Potier, S., Saurin, W., Tekala, F., Torfani-Nioche, C., Wesolowski-Louvel, M., Wincker, P., and Wilson, R.	A set of genomic clones for the hemiascomycetous yeasts: 1. A set of genomic clones for molecular evolution studies	FEBS LETT. 487 (1), 3-12 (2000)

1	11152876	
2	(bases 1 to 759)	
CASAREGOLA, S., NUOVEGLISE, C., LEPINGLE, A., BON, E., FEYEROL, C.,		
ARTIGUENAVE, F., MINCKER, P. and GALLARDIN, C.		
AUTHORS		
TITLE		
Genomic exploration of the nematascytous yeasts: 17. Yarrowia		
lipolytica		
polyploica		
JOURNAL		
FEBS 2892. 487 (1), 95-100 (2000)		
11152892		
3	(bases 1 to 759)	
REFERENCE		

ANALYST	AUTHORS	TITLE	JOURNAL	COMMENT
		Genoscope. Direct Submission Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail sef@genoscope.cns.fr - Web : www.genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>uvarum</i> , <i>Saccharomyces</i> <i>exiguus</i> , <i>Saccharomyces servazzii</i> , <i>Zygosaccharomyces rouxii</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces</i> <i>lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Pichia</i> <i>angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 kb 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.		





Query Match 5.2%; Score 46.2; DB 4; Length 2565;  
 Best Local Similarity 50.7%; Pred. No. 0.42;  
 Matches 111; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

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 QY 715 TTGAGAAATTAAGATGTTGATTCGAGAGTGGCAGATAGATTGAAAATACAGAAAT 774  
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 DB 718 CAGACTATATACATTTAATTTTAACTGACAGACAGACAGAGTTGCTAAAGAAATTTAA 659  
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## RESULT 15

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 sequence.  
 ACCESSION AG311217  
 VERSION AG311217.1 GI:47884171  
 KEYWORDS GSS.  
 SOURCE Mus musculus molossinus (Japanese wild mouse)  
 ORGANISM Mus musculus molossinus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,  
 Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriaki, K. and  
 Shiroishi, T.  
 Contribution of Asian mouse subspecies Mus musculus molossinus to  
 genomic constitution of strain C57BL/6J, as defined by BAC-end  
 sequence-SNP analysis  
 Genome Res. 14 (12), 2439-2447 (2004)

TITLE  
 15574823  
 2 (bases 1 to 1514)  
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
 Direct Submission  
 Submitted (17-NOV-2003) Maehira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa, 230-0045, Japan  
 (E-mail: hattori@gsc.riken.jp, URL: http://hgpc.gsc.riken.go.jp/,  
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
 Clones are derived from the mouse BAC library MSMg01. For BAC  
 library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
 Tsukuba Institute Bio Resource Center,  
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
 Koyadai, Tsukuba, 305-0074 Japan  
 phone: 81-298-36-9189, fax: 81-298-36-9199  
 e-mail: abe@rtc.riken.jp

## COMMENT

PRIMERS  
 Sequencing : T7

## LIBRARY

Vector : pBACE3.6  
 R.Site 1 : EcoRI  
 R.Site 2 : EcoRI.

## FEATURES

source

1. .1514  
 /organism="Mus musculus molossinus"  
 /mol\_type="genomic DNA"  
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 /sex="male"  
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ORIGIN  
 Query Match 5.1%; Score 45.6; DB 10; Length 1514;  
 Best Local Similarity 52.7%; Pred. No. 0.54;  
 Matches 99; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

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 DB 702 AGAAATATATAAAAAAATAAAATGAAATGAATAAAAAAATAAATAATATATAATGAAAAAG 643  
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 QY 806 TACAACCTATTGCTTGAAGTAGAACAAGAGATAAGAACTTTCTGTTTCAGCTTATTTAAT 865  
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 QY 866 GATAAAAA 873  
 DB 522 AAAAAAA 515

Search completed: March 8, 2006, 04:47:23  
 Job time : 4491.83 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
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Run on: March 7, 2006, 22:34:28; Search time 297.125 Seconds  
(without alignments)  
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Perfect score: 888  
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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0  
Searched: 1303057 seqs, 888780828 residues  
Total number of hits satisfying chosen parameters: 2606114

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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
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2: /cgn2\_6/ptodata/1/ina/5 COMB.seq:  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:  
5: /cgn2\_6/ptodata/1/ina/6 COMB.seq:  
6: /cgn2\_6/ptodata/1/ina/PCRB COMB.seq:  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:  
9: /cgn2\_6/ptodata/1/ina/backfiles.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	888	100.0	888	3	US-09-506-286B-57
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3	886.4	99.8	891	3	US-09-506-286B-50
4	886.4	99.8	891	3	US-10-065-133A-50
5	884.4	99.6	888	3	US-09-506-286B-53
6	884.4	99.6	888	3	US-10-065-133A-53
7	706.4	79.5	906	3	US-10-204-664A-6
8	690	77.7	690	3	US-09-506-286B-52
9	690	77.7	690	3	US-09-506-286B-59
10	690	77.7	690	3	US-10-065-133A-52
11	690	77.7	690	3	US-10-065-133A-59
12	463.4	52.2	468	3	US-09-506-286B-54
13	463.4	52.2	468	3	US-10-065-133A-54
14	291.4	32.8	293	3	US-09-506-286B-56
15	291.4	32.8	293	3	US-10-065-133A-56
16	212.8	24.0	918	6	PCT-US94-01149-9
17	212.8	24.0	918	6	PCT-US94-01149-58
18	212	23.9	453	2	US-08-388-267C-3
19	212	23.9	453	3	US-09-277-720-3
20	212	23.9	690	6	PCT-US94-01149-11
21	212	23.9	690	6	PCT-US94-01149-71
22	212	23.9	924	6	PCT-US94-01149-15
23	211.6	23.8	681	6	PCT-US94-01149-25
24	211.6	23.8	717	6	PCT-US94-01149-23

25	211.6	23.8	729	6	PCT-US94-01149-17
26	211.6	23.8	912	6	PCT-US94-01149-31
27	210.4	23.7	1014	2	US-08-441-857-7
28	210.4	23.7	1014	3	US-08-193-159-7
29	210.4	23.7	1014	3	US-08-283-646C-7
30	210.4	23.7	1017	2	US-08-441-857-9
31	210.4	23.7	1017	2	US-08-441-857-11
32	210.4	23.7	1017	3	US-08-193-159-9
33	210.4	23.7	1017	3	US-08-283-646C-9
34	210.4	23.7	1017	3	US-08-283-646C-11
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37	210.4	23.7	1020	3	US-08-283-646C-5
38	210.4	23.7	915	6	PCT-US94-01149-56
39	208.8	23.5	7616	6	PCT-US94-01149-54
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45	42.4	4.8	601	3	US-09-949-016-184382

ALIGNMENTS

RESULT 1  
US-09-506-286B-57  
; Sequence 57, Application US/09506286B  
; Patent No. 6482414  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: The University of Pittsburgh, of the Commonwealth  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2  
; CURRENT APPLICATION NUMBER: US/09/506,286B  
; CURRENT FILING DATE: 2000-02-16  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 57  
; LENGTH: 888  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (27)..(716)  
US-09-506-286B-57

Query Match	100.0%;	Score 888;	DB 3;	Length 888;
Best Local Similarity	100.0%;	Pred. No. 2.3e-252;	Mismatches 0;	Indels 0;
Matches 888;	Conservative 0;			
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Db	61	ACTGTTTCTTTGGCATGTCGCAAAACGATTTGCAGACCAAGAACTGGGTGATGCCCAT	120	
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RESULT 2  
US-10-065-133A-57  
; Sequence 57, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 57  
; LENGTH: 888  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (27)..(716)  
; OTHER INFORMATION:  
US-10-065-133A-57  
Query Match 100.0%; Score 888; DB 3; Length 888;

Best Local Similarity 100.0%; Pred. No. 2.3e-252;  
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 3  
US-09-506-286B-50  
; Sequence 50, Application US/09506286B  
; Patent No. 6482414  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES



FILE REFERENCE: EQ-1-C2  
CURRENT APPLICATION NUMBER: US/09/506,286B  
CURRENT FILING DATE: 2000-02-16  
PRIOR APPLICATION NUMBER: 09/133,921  
PRIOR FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: PCT/US99/18583  
PRIOR FILING DATE: 1999-08-12  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 50  
LENGTH: 891  
TYPE: DNA  
ORGANISM: Equine influenza virus H3N8  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (27)..(716)  
US-09-506-286B-50

Query Match 99.8%; Score 886.4; DB 3; Length 891;  
Best Local Similarity 99.9%; Pred. No. 6.7e-252;  
Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB	361	CAGCTCCCTATGTATAGATGTGACCGCAATCATGATAGAAACATCATCTTAAAG	420
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DB 841 ACTTTCCTGCTTTCAGCTTATTAATGATATAAAACACCCCTTGTCTTA 888

RESULT 4  
US-10-065-133A-50  
Sequence 50, Application US/10065133A  
Patent No. 6685946  
GENERAL INFORMATION:  
APPLICANT: Dowling, Patricia W.  
APPLICANT: Youngner, Julius S.  
TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
FILE REFERENCE: EQ-1-C2-1  
CURRENT APPLICATION NUMBER: US/10/065,133A  
CURRENT FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: PCT/US99/18583  
PRIOR FILING DATE: 1999-08-12  
PRIOR APPLICATION NUMBER: 09/133,921  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 50  
LENGTH: 891  
TYPE: DNA  
ORGANISM: Equine influenza virus H3N8  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (27)..(716)  
OTHER INFORMATION:  
US-10-065-133A-50

Query Match 99.8%; Score 886.4; DB 3; Length 891;  
Best Local Similarity 99.9%; Pred. No. 6.7e-252;  
Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	AGCAAAAGCAGGGTGACAAAACATATCGATTCCACACCTGTGTCAAGCTTTCAGGTAG	60
DB	1	AGCAAAAGCAGGGTGACAAAACATATCGATTCCACACCTGTGTCAAGCTTTCAGGTAG	60
QY	61	ACTGTTTCTTTGGCATGTGCGCAAAAGATTTGCGACCAAGAACTGGGTGATGCCCAT	120
DB	61	ACTGTTTCTTTGGCATGTGCGCAAAAGATTTGCGACCAAGAACTGGGTGATGCCCAT	120
QY	121	TCCTTGACCGGCTTCGCCGAGACCAAGTCCCTAAAGGAAGAGGTAGTCTTGGTC	180
DB	121	TCCTTGACCGGCTTCGCCGAGACCAAGTCCCTAAAGGAAGAGGTAGTCTTGGTC	180
QY	181	TGACATCGAAACAGCCACTGTGCGAGGAAGCAGATAGTGGAGAGATTTGGAGAGG	240
DB	181	TGACATCGAAACAGCCACTGTGCGAGGAAGCAGATAGTGGAGAGATTTGGAGAGG	240
QY	241	AATCAGATGAGGCACTTAAATGACCAATTCGCTCTGTCTGCTTCAAGCTTAACTG	300
DB	241	AATCAGATGAGGCACTTAAATGACCAATTCGCTCTGTCTGCTTCAAGCTTAACTG	300
QY	301	ACATGACTCTTGGATGTCAAGAGACTGGTTCATGCTCATGCCCAAGCAAGATTA	360
DB	301	ACATGACTCTTGGATGTCAAGAGACTGGTTCATGCTCATGCCCAAGCAAGATTA	360
QY	361	CAGCTCCCTATGTATAGATGTGACCGCAATCATGATAGAAACATCATCTTAAAG	420
DB	361	CAGCTCCCTATGTATAGATGTGACCGCAATCATGATAGAAACATCATCTTAAAG	420
QY	421	CAAACTTTAGTGTGATTTTGAAGAGTGGCAATCATGATAGAAACATCATCTTAAAG	480
DB	421	CAAACTTTAGTGTGATTTTGAAGAGTGGCAATCATGATAGAAACATCATCTTAAAG	480

481 AAGAGGAGCAGTCGTTGGCGAAATTTCAACATTCGCTTCTCTCCAGGACATCTAATG 540  
Db |  
481 AAGAGGAGCAGTCGTTGGCGAAATTTCAACATTCGCTTCTCTCCAGGACATCTAATG 540  
Qy |  
541 AGGATGTCAAAATGCAATTTGGGTCCTCATCGGAGGACTTAAATGGATGATTAACGG 600  
Db |  
541 AGGATGTCAAAATGCAATTTGGGTCCTCATCGGAGGACTTAAATGGATGATTAACGG 600  
Qy |  
601 TTAGAAATCTCTGAACTCTACAGAGATTCGTTGGAGAAAGCAGTCTAGAGATGGGAGAC 660  
Db |  
601 TTAGAAATCTCTGAACTCTACAGAGATTCGTTGGAGAAAGCAGTCTAGAGATGGGAGAC 660  
Qy |  
661 CTTCAATTCCTCCAAAGCAGAAACGAAATTTGGAGAAACAAATTCGAGCCAGAGTTTGA 720  
Db |  
661 CTTCAATTCCTCCAAAGCAGAAACGAAATTTGGAGAAACAAATTCGAGCCAGAGTTTGA 720  
Qy |  
721 GAAATAGATGTTGATTGAAGAGTGGGACATAGATTGAAATATACAGAAATPAGTTT 780  
Db |  
721 GAAATAGATGTTGATTGAAGAGTGGGACATAGATTGAAATATACAGAAATPAGTTT 780  
Qy |  
781 GRACAAATACATTTATGCAAGCCTTACAACTATTGCTTGAAGTAGAAACAAGAGATAAG 840  
Db |  
781 GRACAAATACATTTATGCAAGCCTTACAACTATTGCTTGAAGTAGAAACAAGAGATAAG 840  
Qy |  
841 ACTTCTGCTTTCAGCTTATTAAATGATAAAACACCCCTTGTCTTA 888  
Db |  
841 ACTTCTGCTTTCAGCTTATTAAATGATAAAACACCCCTTGTCTTA 888

RESULT 5  
US-09-506-286B-53  
; Sequence 53, Application US/09506286B  
; Patent No. 6482414  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; APPLICANT: The University of Pittsburgh, of the Commonwealth  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2  
; CURRENT APPLICATION NUMBER: US/09/506,286B  
; PRIOR FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 53  
; TYPE: DNA  
; LENGTH: 888  
; ORGANISM: Equine influenza virus H3N8  
US-09-506-286B-53

Query Match 99.6%; Score 884.4; DB 3; Length 888;  
Best Local Similarity 99.9%; Pred. No. 2.6e-251;  
Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAAAAGCAGGTCACAAAACATAATGGATTCCAACTGTGTCAAGCTTCAGGTAGAC 62  
Db 1 CAAAAGCAGGTCACAAAACATAATGGATTCCAACTGTGTCAAGCTTCAGGTAGAC 60  
Qy 63 TGTGTTCTTTTGGCATGTCCGCAACGATTTGCAAGCAAGAACTGGGTGATGCCCATTC 122  
Db 61 TGTGTTCTTTTGGCATGTCCGCAACGATTTGCAAGCAAGAACTGGGTGATGCCCATTC 120  
Qy 123 CTTGACCGGCTTCCCGAGACAGAGTCCCTAAAGGAGAGGTAGACATCTTTGGTCTG 182  
Db 121 CTTGACCGGCTTCCCGAGACAGAGTCCCTAAAGGAGAGGTAGACATCTTTGGTCTG 180  
Qy 183 GACATCGAAACAGCCACTCGTGCAGGAAAGCAGATAGTGGAGAGATCTCGAAGAGGAA 242  
Db 181 GACATCGAAACAGCCACTCGTGCAGGAAAGCAGATAGTGGAGAGATCTCGAAGAGGAA 240

243 TCAGATGAGGACCTTAAAAATGACCAATTCGCTTCTGTTCTCTCCAGTACTTAACCTGAC 302  
Db |  
241 TCAGATGAGGACCTTAAAAATGACCAATTCGCTTCTGTTCTCTCCAGTACTTAACCTGAC 300  
Qy |  
303 ATGACTCTTGTATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCCAGCAGAAAGTAACA 362  
Db |  
301 ATGACTCTTGTATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCCAGCAGAAAGTAACA 360  
Qy |  
363 GGTCTCCCTATGTATAAGAAATGGACAGGCAATCATGGATAAGAAACATCATCTTTAAAGCA 422  
Db |  
361 GGTCTCCCTATGTATAAGAAATGGACAGGCAATCATGGATAAGAAACATCATCTTTAAAGCA 420  
Qy |  
423 AACTTTAGTGTGATTTTCGAAAGGCTGGAGACATTAATCTACTTTAGAGCCTTCCCGAA 482  
Db |  
421 AACTTTAGTGTGATTTTCGAAAGGCTGGAGACATTAATCTACTTTAGAGCCTTCCCGAA 480  
Qy |  
483 GRAGGAGCAGTCGTTGGCGAAATTTCAACATTCGCTTCTCTCCAGGACATCTAATGAG 542  
Db |  
481 GRAGGAGCAGTCGTTGGCGAAATTTCAACATTCGCTTCTCTCCAGGACATCTAATGAG 540  
Qy |  
543 GATGTCMAAATGCAATTTGGGTCCTCATCGAGAGCTTAAATGGAATGATAATACCGTT 602  
Db |  
541 GATGTCMAAATGCAATTTGGGTCCTCATCGAGAGCTTAAATGGAATGATAATACCGTT 600  
Qy |  
603 AGAATCTCTGAACTCTACAGAGATTCGCTTGGAGAGAGTCTAGAGAAATGGAGACCT 662  
Db |  
601 AGAATCTCTGAACTCTACAGAGATTCGCTTGGAGAGAGTCTAGAGAAATGGAGACCT 660  
Qy |  
663 TCATTCCTCCAAAGCAGAAACGAAATTTGGAGAGAACTTGAAGCAGAACTTTGAAGA 722  
Db |  
661 TCATTCCTCCAAAGCAGAAACGAAATTTGGAGAGAACTTGAAGCAGAACTTTGAAGA 720  
Qy |  
723 AATAAGATGTTGATTGAGAGAGTGGAGATAGATTGAAATACAGAAATAGTTTGA 782  
Db |  
721 AATAAGATGTTGATTGAGAGAGTGGAGATAGATTGAAATACAGAAATAGTTTGA 780  
Qy |  
783 ACAATAACATTTATGAGCCTTCAACTATTCGTTGAAGTGAACAGAGATAAGAAC 842  
Db |  
781 ACAATAACATTTATGAGCCTTCAACTATTCGTTGAAGTGAACAGAGATAAGAAC 840  
Qy |  
843 TTTCTGTTTCAGCTTATTAAATGATAAAACACCCCTTGTCTTA 888  
Db |  
841 TTTCTGTTTCAGCTTATTAAATGATAAAACACCCCTTGTCTTA 886

RESULT 6  
US-10-065-133A-53  
; Sequence 53, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; APPLICANT: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; TITLE OF INVENTION: EQ-1-C2-1  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 53  
; TYPE: DNA  
; LENGTH: 888  
; ORGANISM: Equine influenza virus H3N8  
US-10-065-133A-53

Query Match 99.6%; Score 884.4; DB 3; Length 888;  
Best Local Similarity 99.9%; Pred. No. 2.6e-251;  
Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAAAAGCAGGTCACAAAACATAATGGATTCCAACTGTGTCAAGCTTCAGGTAGAC 62

Db 1 CAAAAGCAGGGTGACAAAACATGATGATTCACACATGTTCAAGCTTTTCAGGTAGAC 60  
Qy TGTTCCTTTTGGCATGTCGCAAAACATTTGACAGCAAGAACTGGGTGATGCCCATTC 122  
Db TGTTCCTTTTGGCATGTCGCAAAACATTTGACAGCAAGAACTGGGTGATGCCCATTC 120  
Qy CTTGACCGGCTTCGCGAGACGAGAGTCCCTTAAAGAGAGAGTGAAGTCTTGGTCTG 182  
Db CTTGACCGGCTTCGCGAGACGAGAGTCCCTTAAAGAGAGAGTGAAGTCTTGGTCTG 180  
Qy GACATGAAACAGCCACTCGTGAGGAAAGAGAGATGATGAGAGAGATTCGGAAGAGAA 242  
Db GACATGAAACAGCCACTCGTGAGGAAAGAGAGATGATGAGAGAGATTCGGAAGAGAA 240  
Qy TCAGATGAGGCACTTAAAGATGACCATTTGCTCTGTTCTCTTTCAGGCTTAACTGAC 302  
Db TCAGATGAGGCACTTAAAGATGACCATTTGCTCTGTTCTCTTTCAGGCTTAACTGAC 300  
Qy ATGACTCTTGATGAGATGTCAGAGAGACTGTTTCATGCTCATGCCCAAGCAGAAAGTAA 362  
Db ATGACTCTTGATGAGATGTCAGAGAGACTGTTTCATGCTCATGCCCAAGCAGAAAGTAA 360  
Qy GGCTCCCTATGTAAGATGAGAGAGGAGGATCATGATGAAGATCATACTTAAAGCA 422  
Db GGCTCCCTATGTAAGATGAGAGAGGAGGATCATGATGAAGATCATACTTAAAGCA 420  
Qy AACTTTAGTGTGATTTGGAAGGCTGGAGACATTAATTAATTAAGGCTTCAACCGAA 482  
Db AACTTTAGTGTGATTTGGAAGGCTGGAGACATTAATTAATTAAGGCTTCAACCGAA 480  
Qy GAAGAGCAGTCTGTTGGCGAAATTTTCCCATTTGCTCTTCCAGGACATTAATGAG 542  
Db GAAGAGCAGTCTGTTGGCGAAATTTTCCCATTTGCTCTTCCAGGACATTAATGAG 540  
Qy GATGTCGAAATGCAATTTGGGCTCTCATCGGAGGACTTAAATGGAATGATTAACGTT 602  
Db GATGTCGAAATGCAATTTGGGCTCTCATCGGAGGACTTAAATGGAATGATTAACGTT 600  
Qy AGAATCTGGAATCTTACAGAGATTCGCTTGGAGAGGAGTCAAGATGAGAGGAGCT 662  
Db AGAATCTGGAATCTTACAGAGATTCGCTTGGAGAGGAGTCAAGATGAGAGGAGCT 660  
Qy TCATTCCTCCAAAGCAGAAACGAAATGAGAGAAATTTGAGCCAGAGTTTGAAGA 722  
Db TCATTCCTCCAAAGCAGAAACGAAATGAGAGAAATTTGAGCCAGAGTTTGAAGA 720  
Qy AATAAGATGTTGATTTGAAGAGTGGCAGATAGATTGAAATGAGAGAAATGATTTGA 782  
Db AATAAGATGTTGATTTGAAGAGTGGCAGATAGATTGAAATGAGAGAAATGATTTGA 780  
Qy ACAAATGATTTATGCAAGCTTTCAACTATGCTTGAAGTGAAGAGAGATTAAGAC 842  
Db ACAAATGATTTATGCAAGCTTTCAACTATGCTTGAAGTGAAGAGAGATTAAGAC 840  
Qy TTTCTGTTTTCAGCTTATTAATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 888  
Db TTTCTGTTTTCAGCTTATTAATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 886

RESULT 7  
US-10-204-664A-6  
; Sequence 6, Application US/10204664A  
; Patent No. 6800288  
; GENERAL INFORMATION:  
; APPLICANT: FERKO, Boris  
; APPLICANT: EGOV, Andre  
; APPLICANT: VOGLAUER, Regina  
; TITLE OF INVENTION: Recombinant Influenza A Viruses  
; FILE REFERENCE: 113529  
; CURRENT APPLICATION NUMBER: US/10/204,664A  
; CURRENT FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: EP 00104338.9

; PRIOR FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 906  
; TYPE: DNA  
; ORGANISM: Influenza A virus /PRNS38  
US-10-204-664A-6  
  
Query Match 79.5%; Score 706.4; DB 3; Length 906;  
Best Local Similarity 88.2%; Pred. No. 1.2e-198;  
Matches 797; Conservative 0; Mismatches 91; Indels 16; Gaps 2;  
  
Qy 1 AGCAAAAGCAGGGTGACAAAACATTAATGATTTCCAACTGTGTCAAGCTTTTCAGGTAG 60  
Db 1 AGCAAAAGCAGGGTGACAAAACATTAATGATTTCCAACTGTGTCAAGCTTTTCAGGTAG 60  
Qy 61 ACTGTTTCTTTGGCATGTCGCAAAACATTTGACAGCAAGAACTGGGTGATGCCCAT 120  
Db 61 ATTGCTTCTTTGGCATGTCGCAAAACATTTGACAGCAAGAACTGTGTGATGCCCAT 120  
Qy 121 TCCTTCACCGGCTTCGCGAG-----ACGAGAGTCCCTTAAAGAGAGAG 165  
Db 121 TCCTTCACCGGCTTCGCGAGTGAATACTAGCTGATCAGAAATCCTTAAAGAGAGAG 180  
Qy 166 GTAGCACTCTTGGTCTGGAATCGAAACAGCCACTCGTGTGAGGAAAGAGATGTGAGC 225  
Db 181 GCAGCACTCTTGGTCTGGAATCGGAATCGCAAGCCACTCGTGTGAGGAAAGAGATGTGAGC 240  
Qy 226 AGATTTCTGGAAGAGGAGATTCAGATGAGGCACTTTAAATGACCAATTCCTGTTCTGCTT 285  
Db 241 GGAATCTGGAAGAGGAGATTCAGATGAGGCACTTTAAATGACCAATTCCTGTTCTGCTT 300  
Qy 286 CAGCTTACTTAACTGACATGACTTGTGATGAGATGTCAGAGAGTGTGTTTCATGCTCATGC 345  
Db 301 CGGTTTACTTAACTGACATGACTTGTGAGGAAATGTCAGAGGAGTGTGTTCCATGCTCATAC 360  
Qy 346 CCAGCAGAGAGTAACTAGGCTCCCTATGTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 404  
Db 361 CCAGCAGAGAGTAACTAGGCTCCCTATGTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
Qy 405 AACATCATCTTAAAGCAAACTTTAGTGTGATTTTGAAGAGGCTGAGAGACATAAATACTA 464  
Db 421 AACATCATCTTAAAGCAAACTTTAGTGTGATTTTGAAGAGGCTGAGAGACATAAATACTA 480  
Qy 465 CTTAGAGCCTTCCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 524  
Db 481 CTAAGGCTTTTCCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
Qy 525 CCAGGACATCTAATGAGAGTGTCAAAATGCAATTTGGGGTCTCTCATCGAGAGGAGCTTAAA 584  
Db 541 CCAGGACATCTAATGAGAGTGTCAAAATGCAATTTGGGGTCTCTCATCGAGAGGAGCTTAAA 600  
Qy 585 TGAATCATTAATGAGTGTGAGATCTCTGAACTCTTACAGATTCCTGTTGAGAGAGAGT 644  
Db 601 TGAATCATTAATGAGTGTGAGATCTCTGAACTCTTACAGATTCCTGTTGAGAGAGAGT 660  
Qy 645 CATGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 704  
Db 661 AATGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
Qy 705 GAGCAGAGAGTGTGAAGAAATTAAGATGTTGAGAGAGTGTGAAGAGAGGAGGAGGAGGAGGAG 764  
Db 721 AGGTCAAGAGTGTGAAGAAATTAAGATGTTGAGAGAGTGTGAAGAGAGGAGGAGGAGGAGGAG 780  
Qy 765 TACAGAGAGATGTTTGAAGCAAAATTAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 824  
Db 781 AACAGAGATGTTTGAAGCAAAATTAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
Qy 825 AGAACAAGAGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 884  
Db 841 GGAGCAGAGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900

us-10-734-373-57.rni

Wed Mar 8 09:11:18 2006

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Qy 885 TCTA 888
Db 901 TCTA 904

RESULT 8
US-09-506-286B-52
; Sequence 52, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-52

Query Match 77.7%; Score 690; DB 3; Length 690;
Best Local Similarity 100.0%; Pred. No. 7.5e-194;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ATGGATTCCAAACACTGCTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 86
Db 1 ATGGATTCCAAACACTGCTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 60

Qy 87 CGATTTCGAGACCAAGAACTCGGTGATGCCCATTCCTTTGACCGGCTTCGCCGAGACCA 146
Db 61 CGATTTCGAGACCAAGAACTCGGTGATGCCCATTCCTTTGACCGGCTTCGCCGAGACCA 120

Qy 147 AAGTCCCTTAAAGAGAGGTAGACACTCTTGGTCTGGACATCGAAACAGCCACTCTGTGA 206
Db 121 AAGTCCCTTAAAGAGAGGTAGACACTCTTGGTCTGGACATCGAAACAGCCACTCTGTGA 180

Qy 207 GGAAGCAGATGTGGAGCAGATTCGGAAGAGGAATCAGATGAGGCACTTAAATGACC 266
Db 181 GGAAGCAGATGTGGAGCAGATTCGGAAGAGGAATCAGATGAGGCACTTAAATGACC 240

Qy 267 ATTGCTCTGTTCTGCTTCAAGCTTAACTGACATGACACTCTTGTATGATGAGTCAAGA 326
Db 241 ATTGCTCTGTTCTGCTTCAAGCTTAACTGACATGACACTCTTGTATGATGAGTCAAGA 300

Qy 327 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAATGGAC 386
Db 301 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAATGGAC 360

Qy 387 CAGGCAATCATGGATTAAGACATCATCTTAAGCAAACTTTAGTGTGATTTTCAAGAGG 446
Db 361 CAGGCAATCATGGATTAAGACATCATCTTAAGCAAACTTTAGTGTGATTTTCAAGAGG 420

Qy 447 CTGGAGACATAAATACTACTTAGAGCTTCAAGCAAGGAGGAGCTGTTGGGCAATT 506
Db 421 CTGGAGACATAAATACTACTTAGAGCTTCAAGCAAGGAGGAGCTGTTGGGCAATT 480

Qy 507 TCACCAATGCGCTTCTCTTCAGGACATTAATGAGTGTCAAAATGCAATTTGGGTC 566
Db 481 TCACCAATGCGCTTCTCTTCAGGACATTAATGAGTGTCAAAATGCAATTTGGGTC 540

Qy 567 CTCATCGGAGGACTTAAATGGAATGATACGTTGAGTCTTGAACACTCTACAGA 626
Db 541 CTCATCGGAGGACTTAAATGGAATGATACGTTGAGTCTTGAACACTCTACAGA 600

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Qy 627 TTTCGCTTGGAGAGAGAGTCTATGAGAAATCGGAGACCTTCAATCCCTCCAAAGCAAAACGA 686
Db 601 TTTCGCTTGGAGAGAGAGTCTATGAGAAATCGGAGACCTTCAATCCCTCCAAAGCAAAACGA 660

Qy 687 AAAATGGAGAGAAACAAATGAGCCAGAGTT 716
Db 661 AAAATGGAGAGAAACAAATGAGCCAGAGTT 690

RESULT 9
US-09-506-286B-59
; Sequence 59, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-59

Query Match 77.7%; Score 690; DB 3; Length 690;
Best Local Similarity 100.0%; Pred. No. 7.5e-194;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ATGGATTCCAAACACTGCTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 86
Db 1 ATGGATTCCAAACACTGCTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 60

Qy 87 CGATTTCGAGACCAAGAACTCGGTGATGCCCATTCCTTTGACCGGCTTCGCCGAGACCA 146
Db 61 CGATTTCGAGACCAAGAACTCGGTGATGCCCATTCCTTTGACCGGCTTCGCCGAGACCA 120

Qy 147 AAGTCCCTTAAAGAGAGGTAGACACTCTTGGTCTGGACATCGAAACAGCCACTCTGTGA 206
Db 121 AAGTCCCTTAAAGAGAGGTAGACACTCTTGGTCTGGACATCGAAACAGCCACTCTGTGA 180

Qy 207 GGAAGCAGATGTGGAGCAGATTCGGAAGAGGAATCAGATGAGGCACTTAAATGACC 266
Db 181 GGAAGCAGATGTGGAGCAGATTCGGAAGAGGAATCAGATGAGGCACTTAAATGACC 240

Qy 267 ATTGCTCTGTTCTGCTTCAAGCTTAACTGACATGACACTCTTGTATGATGAGTCAAGA 326
Db 241 ATTGCTCTGTTCTGCTTCAAGCTTAACTGACATGACACTCTTGTATGATGAGTCAAGA 300

Qy 327 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAATGGAC 386
Db 301 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAATGGAC 360

Qy 387 CAGGCAATCATGGATTAAGACATCATCTTAAGCAAACTTTAGTGTGATTTTCAAGAGG 446
Db 361 CAGGCAATCATGGATTAAGACATCATCTTAAGCAAACTTTAGTGTGATTTTCAAGAGG 420

Qy 447 CTGGAGACATAAATACTACTTAGAGCTTCAAGCAAGGAGGAGCTGTTGGGCAATT 506
Db 421 CTGGAGACATAAATACTACTTAGAGCTTCAAGCAAGGAGGAGCTGTTGGGCAATT 480

Qy 507 TCACCAATGCGCTTCTCTTCAGGACATTAATGAGTGTCAAAATGCAATTTGGGTC 566
Db 481 TCACCAATGCGCTTCTCTTCAGGACATTAATGAGTGTCAAAATGCAATTTGGGTC 540

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567	QY	CTCATCGGAGGACCTTAATATGGAATGATAATATACGGTTAGAACTCTCTGAACTCTACAGAGA	626
541	Db	CTCATCGGAGGACCTTAATATGGAATGATAATATACGGTTAGAACTCTCTGAACTCTACAGAGA	600
627	QY	TTTCGCTTTGGAGAGCAGTCAATGAGAAATGGGAGACCTTCAATTCCTCTCAAGCAGAAACGA	686
601	Db	TTTCGCTTTGGAGAGCAGTCAATGAGAAATGGGAGACCTTCAATTCCTCTCAAGCAGAAACGA	660
687	QY	AAAAATGGGAGAGAACAAATTCGAGCCAGAAAGTT	716
661	Db	AAAAATGGGAGAGAACAAATTCGAGCCAGAAAGTT	690

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RESULT 10
US-10-065-133A-52
; Sequence 52, Application US/10065133A
; Patent NO. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C-21
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-52

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Query Match	77.7%	Score 690;	DB 3;	Length 690;
Best Local Similarity	100.0%;	Pred. No. 7.5e-194;		
Matches 690;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	27	ATGGAATCCACACACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTTGGCATGTCGCGAAA	86	
Db	1	ATGGAATCCACACACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTTGGCATGTCGCGAAA	60	
QY	87	CGAATTTGCAGACCAAGAACTGGGTGATGCCCAATCTCTTGACCGGCTTCGCCGAGACGAC	146	
Db	61	CGAATTTGCAGACCAAGAACTGGGTGATGCCCAATCTCTTGACCGGCTTCGCCGAGACGAC	120	
QY	147	AAGTCCCTTAAAGGAGAGGTAGCAGCTTTGGTCTGGACATCCGAACAGGCACCTCGTGCA	206	
Db	121	AAGTCCCTTAAAGGAGAGGTAGCAGCTTTGGTCTGGACATCCGAACAGGCACCTCGTGCA	180	
QY	207	GGAAAGCAGATAGTGGACAGATTTCTGGAAGAGGAATCAGATGAGGCATCTTAAATGACC	266	
Db	181	GGAAAGCAGATAGTGGACAGATTTCTGGAAGAGGAATCAGATGAGGCATCTTAAATGACC	240	
QY	267	ATTGGCTCTGTTCTCTGTTCAAGCTTACTTAACTGACATGACTCTTGTATGAGATGTCNAGA	326	
Db	241	ATTGGCTCTGTTCTCTGTTCAAGCTTACTTAACTGACATGACTCTTGTATGAGATGTCNAGA	300	
QY	327	GACTGTTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAAGAATGGAC	386	
Db	301	GACTGTTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAAGAATGGAC	360	
QY	387	CAGGCATCTAGGTAAGAGACATATCTTAAAGCAACACTTAGTGTGATGTTTTGGAAGG	446	
Db	361	CAGGCATCTAGGTAAGAGACATATCTTAAAGCAACACTTAGTGTGATGTTTTGGAAGG	420	
QY	447	CTGGAGACACTATATCTATCTTAGAGCCTTCACCGAAGAGGACGAGCTCGTTGGCGAAATT	506	
Db	421	CTGGAGACACTATATCTATCTTAGAGCCTTCACCGAAGAGGACGAGCTCGTTGGCGAAATT	480	
QY	507	TCACCAATTCGCCTCTCTTCCAGGACATATCTAATGAGGATGTCAAAAATGCAATTTGGGGTC	566	

Db	481		TCACATTGCCCTCTCTTCCAGGACATACCTAATGAGGATGTCAAAATGCATTTGGGGTC	540
Qy	567	CTCATCGGAGGACCTAAATGGAATGAATAATACGGTTAGAACTCTGAAACTCTACAGAGA	626	
Db	541	CTCATCGGAGGACCTAAATGGAATGAATAATACGGTTAGAACTCTGAAACTCTACAGAGA	600	
Qy	627	TTCGCTTGGAGAGCAGCTCATGAGAAATGGGAGACCTTCATTCCCTCCAAAGCAGAAACGA	686	
Db	601	TTCGCTTGGAGAGCAGCTCATGAGAAATGGGAGACCTTCATTCCCTCCAAAGCAGAAACGA	660	
Qy	687	AAATGGGAGAGCAATTTGAGCCAGAGTT	716	
Db	661	AAATGGGAGAGCAATTTGAGCCAGAGTT	690	

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RESULT 11
US-10-065-133A-59
  ; Sequence 59, Application US/10065133A
  ; Patent NO. 6685946
  ; GENERAL INFORMATION:
  ; APPLICANT: Dowling, Patricia W.
  ; APPLICANT: Youngner, Julius S.
  ; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
  ; FILE REFERENCE: EQ-1-C2-1
  ; CURRENT APPLICATION NUMBER: US/10/065,133A
  ; CURRENT FILING DATE: 2002-12-10
  ; PRIOR APPLICATION NUMBER: PCT/US99/18583
  ; PRIOR FILING DATE: 1999-08-12
  ; PRIOR APPLICATION NUMBER: 09/133,921
  ; PRIOR FILING DATE: 1998-08-13
  ; NUMBER OF SEQ ID NOS: 108
  ; SOFTWARE: PatentIn version 3.1
  ; SEQ ID NO 59
  ; LENGTH: 690
  ; TYPE: DNA
  ; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-59

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Query Match	77.7%	Score 690;	DB 3;	Length 690;
Best Local Similarity	100.0%;	Pred. No. 7.5e-194;		
Matches 690;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	27	ATGGATTCACAACACTGTGTCAAGCTTTTCAGGTAGACATGTTTTCCTTTGGCAGATGTCGCAAA	86	
DB	1	ATGGATTCACAACACTGTGTCAAGCTTTTCAGGTAGACATGTTTTCCTTTGGCAGATGTCGCAAA	60	
QY	87	CGATTTCGAGACCAAGAACTGGGTGATGCCCACTTCCTTTGACCGGCTTCGCCGAGACCAG	146	
DB	61	CGATTTCGAGACCAAGAACTGGGTGATGCCCACTTCCTTTGACCGGCTTCGCCGAGACCAG	120	
QY	147	AAGTCCCTAAAAGGAAGAGGTAGACACTCTTGGTCTGGACATCGAAAACAGCACTCTGTGCA	206	
DB	121	AAGTCCCTAAAAGGAAGAGGTAGACACTCTTGGTCTGGACATCGAAAACAGCACTCTGTGCA	180	
QY	207	GGAAAGCAGATAGTGGAGCAGAGATTCTGGAAGAGGAATCAGATGAGGCACCTTAAATGACC	266	
DB	181	GGAAAGCAGATAGTGGAGCAGAGATTCTGGAAGAGGAATCAGATGAGGCACCTTAAATGACC	240	
QY	267	ATTGCCTCTGTTCTCTCTCTTCACGCTACTTAACTAGCATGACTCTTGATCAGATGTCGAAGA	326	
DB	241	ATTGCCTCTGTTCTCTCTCTCTTCACGCTACTTAACTAGCATGACTCTTGATGAGATGTCGAAGA	300	
QY	327	GACTGGTTCATGCTCATGCCCCAGCAGAAAGTAAACGGCTCCCTATGTTATAGAAATGGAC	386	
DB	301	GACTGGTTCATGCTCATGCCCCAGCAGAAAGTAAACAGGCTCCCTATGTTATAGAAATGGAC	360	
QY	387	CAGGCAATCATGTCATAGGAACATCATACTTAAAGCAAACTTTAGTGTGATTTTCGAAGG	446	
DB	361	CAGGCAATCATGTCATAGGAACATCATACTTAAAGCAAACTTTAGTGTGATTTTCGAAGG	420	
QY	447	CTGGAGACACTAATATCTACTTTAGAGCCCTTCACCGAAGAGGAGCAGCTCGTTGGCGAAATTT	506	

Db 421 CTGGAGACATAAATACTACTTAGAGCCTTCAACGAAGAGGACAGTCGTTGGCGAAATT 480  
Qy 507 TCACCAATTCCTCTCTTCCAGGACATACTAATAGAGATGTCAAAATGCAATTTGGGTC 566  
Db 481 TCACCAATTCCTCTCTTCCAGGACATACTAATAGAGATGTCAAAATGCAATTTGGGTC 540  
Qy 567 CTCATCGGAGGACTTAAATGGAATGATAATACGTTAGAACTCTTGAACTCTACAGAGA 626  
Db 541 CTCATCGGAGGACTTAAATGGAATGATAATACGTTAGAACTCTTGAACTCTACAGAGA 600  
Qy 627 TTCGCTTCGAGAGCACTCATGAGATGGGAGACCTTCATTCCTCCAAAGCAGAAACGA 686  
Db 601 TTCGCTTCGAGAGCACTCATGAGATGGGAGACCTTCATTCCTCCAAAGCAGAAACGA 660  
Qy 687 AATATGGAGAGCAATTTGAGCCAGAGTT 716  
Db 661 AATATGGAGAGCAATTTGAGCCAGAGTT 690

RESULT 12  
US-09-506-286B-54  
; Sequence 54, Application US/09506286B  
; Patent No. 8482411  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Younger, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2  
; CURRENT APPLICATION NUMBER: US/09/506,286B  
; PRIOR FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: PCI/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 54  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3)..(293)  
US-09-506-286B-54

Query Match 52.2%; Score 463.4; DB 3; Length 468;  
Best Local Similarity 99.8%; Pred. No. 6.6e-127;  
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 424 ACTTTAGTGTGATTTTCGAAAGCTGGAGACATACTACTTAGAGCCTTCACCGAG 483  
Db 1 ACTTTAGTGTGATTTTCGAAAGCTGGAGACATACTACTTAGAGCCTTCACCGAG 60  
Qy 484 AAGGAGCAGTCGTTGGCGAAATTTCAACATTCCTCTCCAGGACATACTAATGAG 543  
Db 61 AAGGAGCAGTCGTTGGCGAAATTTCAACATTCCTCTCCAGGACATACTAATGAG 120  
Qy 544 ATGTCAAAATGCAATTTGGGGTCTCATCGAGACTTAAATGGAATGATATACGGTTA 603  
Db 121 ATGTCAAAATGCAATTTGGGGTCTCATCGAGACTTAAATGGAATGATATACGGTTA 180  
Qy 604 GAATCTCTGAACTCTACAGAGATTCGCTTCGAGAGCAGTCATGAGATGGGAGCCTT 663  
Db 181 GAATCTCTGAACTCTACAGAGATTCGCTTCGAGAGCAGTCATGAGATGGGAGCCTT 240  
Qy 664 CATTCCTCCAAAGCAGAAACGAAATTTGGAGAGACAAATTGAGCCAGAGTTTGAAGAA 723  
Db 241 CATTCCTCCAAAGCAGAAACGAAATTTGGAGAGACAAATTGAGCCAGAGTTTGAAGAA 300  
Qy 724 ATAAGATGTTGATTGAAAGAGTGGCAGATAGATTGAAAATACGAAATAGTTTGA 783  
Db 301 ATAAGATGTTGATTGAAAGAGTGGCAGATAGATTGAAAATACGAAATAGTTTGA 360  
Qy 843 CAATAAATATTTATGCAAGCTTACAACTTATTCCTCAAGTATGAAATAGTTTGA 888  
Db 421 TTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTA 465

Qy 784 CAATAAATATTTATGCAAGCTTACAACTTATTCCTTGAAGTAAACAGAGATAGAACT 843  
Db 361 CAATAAATATTTATGCAAGCTTACAACTTATTCCTTGAAGTAAACAGAGATAGAACT 420  
Qy 844 TTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTA 888  
Db 421 TTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTA 465

RESULT 13  
US-10-065-133A-54  
; Sequence 54, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Younger, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; PRIOR FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 54  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3)..(293)  
; OTHER INFORMATION:  
US-10-065-133A-54

Query Match 52.2%; Score 463.4; DB 3; Length 468;  
Best Local Similarity 99.8%; Pred. No. 6.6e-127;  
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 424 ACTTTAGTGTGATTTTCGAAAGCTGGAGACATACTACTTAGAGCCTTCACCGAG 483  
Db 1 ACTTTAGTGTGATTTTCGAAAGCTGGAGACATACTACTTAGAGCCTTCACCGAG 60  
Qy 484 AAGGAGCAGTCGTTGGCGAAATTTCAACATTCCTCTCCAGGACATACTAATGAG 543  
Db 61 AAGGAGCAGTCGTTGGCGAAATTTCAACATTCCTCTCCAGGACATACTAATGAG 120  
Qy 544 ATGTCAAAATGCAATTTGGGGTCTCATCGAGACTTAAATGGAATGATATACGGTTA 603  
Db 121 ATGTCAAAATGCAATTTGGGGTCTCATCGAGACTTAAATGGAATGATATACGGTTA 180  
Qy 604 GAATCTCTGAACTCTACAGAGATTCGCTTCGAGAGCAGTCATGAGATGGGAGCCTT 663  
Db 181 GAATCTCTGAACTCTACAGAGATTCGCTTCGAGAGCAGTCATGAGATGGGAGCCTT 240  
Qy 664 CATTCCTCCAAAGCAGAAACGAAATTTGGAGAGACAAATTGAGCCAGAGTTTGAAGAA 723  
Db 241 CATTCCTCCAAAGCAGAAACGAAATTTGGAGAGACAAATTGAGCCAGAGTTTGAAGAA 300  
Qy 724 ATAAGATGTTGATTGAAAGAGTGGCAGATAGATTGAAAATACGAAATAGTTTGA 783  
Db 301 ATAAGATGTTGATTGAAAGAGTGGCAGATAGATTGAAAATACGAAATAGTTTGA 360  
Qy 843 CAATAAATATTTATGCAAGCTTACAACTTATTCCTCAAGTATGAAATAGTTTGA 888  
Db 361 CAATAAATATTTATGCAAGCTTACAACTTATTCCTCAAGTATGAAATAGTTTGA 420  
Qy 844 TTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTA 888  
Db 421 TTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTA 465

## RESULT 14

US-09-506-286B-56  
; Sequence 56, Application US/09506286B  
; Patent No. 6482414  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: The University of Pittsburgh, of the Commonwealth  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2  
; CURRENT APPLICATION NUMBER: US/09/506,286B  
; PRIOR FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 56  
; LENGTH: 293  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-09-506-286B-56

Query Match 32.8%; Score 291.4; DB 3; Length 293;  
Best Local Similarity 99.7%; Pred. No. 4e-76; Indels 0; Gaps 0;  
Matches 292; Conservative 0; Mismatches 1;  
QY 424 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCGAAG 483  
DB 1 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCGAAG 60  
QY 484 AAGGAGCAGTCGTTGGCGAAATTTCCACCATTCGCTTCCAGGAGCAGTCATGAGATGGAGACCTT 543  
DB 61 AAGGAGCAGTCGTTGGCGAAATTTCCACCATTCGCTTCCAGGAGCAGTCATGAGATGGAGACCTT 120  
QY 544 ATGTCAAAAATGCAATTTGGGGTCTCATCGGAGGACTTAAATGGAATGATATACGGTTA 603  
DB 121 ATGTCAAAAATGCAATTTGGGGTCTCATCGGAGGACTTAAATGGAATGATATACGGTTA 180  
QY 604 GAATCTCTGAACACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 663  
DB 181 GAATCTCTGAACACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 240  
QY 564 CATTCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCAGCCAGAGTT 716  
DB 241 CATTCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCAGCCAGAGTT 293

## RESULT 15

US-10-065-133A-56  
; Sequence 56, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; PRIOR FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 56  
; LENGTH: 293  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-10-065-133A-56

Query Match 32.8%; Score 291.4; DB 3; Length 293;  
Best Local Similarity 99.7%; Pred. No. 4e-76; Indels 0; Gaps 0;  
Matches 292; Conservative 0; Mismatches 1;  
QY 424 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCGAAG 483  
DB 1 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCGAAG 60  
QY 484 AAGGAGCAGTCGTTGGCGAAATTTCCACCATTCGCTTCCAGGAGCAGTCATGAGATGGAGACCTT 543  
DB 61 AAGGAGCAGTCGTTGGCGAAATTTCCACCATTCGCTTCCAGGAGCAGTCATGAGATGGAGACCTT 120  
QY 544 ATGTCAAAAATGCAATTTGGGGTCTCATCGGAGGACTTAAATGGAATGATATACGGTTA 603  
DB 121 ATGTCAAAAATGCAATTTGGGGTCTCATCGGAGGACTTAAATGGAATGATATACGGTTA 180  
QY 604 GAATCTCTGAACACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 663  
DB 181 GAATCTCTGAACACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 240  
QY 564 CATTCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCAGCCAGAGTT 716  
DB 241 CATTCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCAGCCAGAGTT 293

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OM nucleic - nucleic search, using sw model

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Perfect score: 888  
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 19587084

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	888	100.0	888	6	US-10-065-133A-57 Sequence 57, Appl
2	888	100.0	888	7	US-10-734-373-57 Sequence 57, Appl
3	888	100.0	888	9	US-10-181-585B-39 Sequence 39, Appl
4	886.4	99.8	891	6	US-10-065-133A-50 Sequence 50, Appl
5	886.4	99.8	891	7	US-10-734-373-50 Sequence 50, Appl
6	886.4	99.8	891	9	US-10-181-585B-32 Sequence 32, Appl
7	884.4	99.6	888	6	US-10-065-133A-53 Sequence 53, Appl
8	884.4	99.6	888	7	US-10-734-373-53 Sequence 53, Appl
9	884.4	99.6	888	9	US-10-181-585B-35 Sequence 35, Appl
10	742.4	83.6	890	8	US-10-855-875-6 Sequence 6, Appl
11	737.6	83.1	890	7	US-10-381-530-8 Sequence 8, Appl
12	692.8	78.0	824	9	US-10-654-737-2 Sequence 2, Appl
13	690	77.7	690	6	US-10-065-133A-52 Sequence 52, Appl
14	690	77.7	690	7	US-10-065-133A-59 Sequence 59, Appl
15	690	77.7	690	9	US-10-734-373-52 Sequence 52, Appl
16	690	77.7	690	7	US-10-734-373-59 Sequence 59, Appl
17	690	77.7	690	9	US-10-181-585B-34 Sequence 34, Appl
18	690	77.7	690	9	US-10-181-585B-41 Sequence 41, Appl
19	684.8	77.1	824	9	US-10-654-737-1 Sequence 1, Appl
20	463.4	52.2	468	6	US-10-065-133A-54 Sequence 54, Appl
21	463.4	52.2	468	7	US-10-734-373-54 Sequence 54, Appl
22	463.4	52.2	468	9	US-10-181-585B-36 Sequence 36, Appl
23	291.4	32.8	293	6	US-10-065-133A-56 Sequence 56, Appl

24	291.4	32.8	293	7	US-10-734-373-56	Sequence 56, Appl
25	291.4	32.8	293	9	US-10-181-585B-38	Sequence 38, Appl
26	209.2	23.6	849	6	US-10-226-872-8	Sequence 8, Appl
27	209.2	23.6	849	6	US-10-226-872-9	Sequence 9, Appl
28	209.2	23.6	849	7	US-10-650-608-8	Sequence 8, Appl
29	209.2	23.6	849	7	US-10-650-608-9	Sequence 9, Appl
30	208.8	23.5	939	6	US-10-312-089-2	Sequence 2, Appl
31	208.8	23.5	939	6	US-10-312-089-4	Sequence 4, Appl
32	103.4	11.6	136	3	US-09-835-694-14	Sequence 14, Appl
33	47	5.3	4257	6	US-10-369-493-46002	Sequence 46002, A
34	44.2	5.0	552	7	US-10-021-323-93	Sequence 93, Appl
35	43	4.8	13361	10	US-11-097-143-24181	Sequence 24181, A
36	43	4.8	3673778	6	US-10-312-841-1	Sequence 1, Appl
37	42.6	4.8	6436	6	US-10-311-455-654	Sequence 654, Appl
38	41.6	4.7	590	5	US-10-027-632-290656	Sequence 290656,
39	41.6	4.7	590	6	US-10-027-632-290656	Sequence 290656,
40	41.4	4.7	640681	3	US-09-790-988-1	Sequence 1, Appl
41	41.2	4.6	647	8	US-10-425-115-40312	Sequence 40312, A
42	41.2	4.6	6076	7	US-10-221-714A-386	Sequence 386, App
43	41.2	4.6	217409	5	US-10-087-192-1954	Sequence 1954, Ap
44	41.2	4.6	3673778	6	US-10-312-841-1	Sequence 1, Appl
45	41	4.6	6351	6	US-10-311-455-1420	Sequence 1420, Ap

## ALIGNMENTS

## RESULT 1

US-10-065-133A-57  
; Sequence 57, Application US/10065133A  
; Publication No. US20030199074A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 57:  
; LENGTH: 888  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (27)..(716)  
; OTHER INFORMATION:  
US-10-065-133A-57

Query Match 100.0%; Score 888; DB 6; Length 888;

Best Local Similarity 100.0%; Pred. No. 3.3e-232;

Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AGCAAAAGCAGGGTGACAAAACATAATGGATTCCCAACACTGTGTCAAGCTTTCAGGTAG	60
Db	1	AGCAAAAGCAGGGTGACAAAACATAATGGATTCCCAACACTGTGTCAAGCTTTCAGGTAG	60
QY	61	ACTGTTTCTTTGGCGGACGACAGAGTTCGAGACCAAGACTGGGTGATGCCCAT	120
Db	61	ACTGTTTCTTTGGCGGACGACAGAGTTCGAGACCAAGACTGGGTGATGCCCAT	120
QY	121	TCCTTGACCGGTTTGGCGGACGACAGAGTTCCTTAAAGAGAGAGTACCTTTGGTC	180
Db	121	TCCTTGACCGGTTTGGCGGACGACAGAGTTCCTTAAAGAGAGAGTACCTTTGGTC	180
QY	181	TGAGCATCGAAACAGCCACTCTGTGAGAGAAAGAGATGTGGAGCAGATTCTTGAAGAGG	240
Db	181	TGAGCATCGAAACAGCCACTCTGTGAGAGAAAGAGATGTGGAGCAGATTCTTGAAGAGG	240

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241 ATTCAGATGAGGCACTTAATAGACCATTCCTGCTGCTTCAAGCTACTTAATG 300  
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Db  
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421 CAAACTTTAGTGTGATTTTCCAAAGGCTGGAGACACTTAATGATGATGATGATGATG 480  
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Qy  
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661 CTTCAATTCCTCCAAAGCAGAAACGAAATGAGAGAACTTAATGATGATGATGATG 720  
Qy  
721 GAAATAGATGTTGATTTGAAGAGAGTGGCAGACATAGATTTGAAATATACAGAAATAG 780  
Db  
721 GAAATAGATGTTGATTTGAAGAGAGTGGCAGACATAGATTTGAAATATACAGAAATAG 780  
Qy  
781 GAAACAATACATTTATGCAAGCCTTACAACTTATGCTTGAAGTAGAACAAGAGATAAGA 840  
Db  
781 GAAACAATACATTTATGCAAGCCTTACAACTTATGCTTGAAGTAGAACAAGAGATAAGA 840  
Qy  
841 ACTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTA 888  
Db  
841 ACTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTA 888

RESULT 2

US-10-734-373-57  
; Sequence 57, Application US/10734373  
; Publication No. US20040137015A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10734,373  
; PRIOR FILING DATE: 2003-12-12  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 57  
; LENGTH: 888  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (27)..(716)  
; OTHER INFORMATION:  
US-10-734-373-57

Query Match 100.0%; Score 888; DB 7; Length 888;  
Best Local Similarity 100.0%; Pred. No. 3.3e-232; Indels 0; Gaps 0;  
Matches 888; Conservative 0; Mismatches 0;  
Qy 1 AGCAAAAGCAGGGGTGACAAACATTAATGATTCCTCAACACTGTGTCAGCTTTCAGGTAG 60  
Db 1 AGCAAAAGCAGGGGTGACAAACATTAATGATTCCTCAACACTGTGTCAGCTTTCAGGTAG 60  
Qy 61 ACTGTTTCTTTGGCTGTCGCAAAACGATTTGGAGACCAAGAACTGGGTGATGCCCAT 120  
Db 61 ACTGTTTCTTTGGCTGTCGCAAAACGATTTGGAGACCAAGAACTGGGTGATGCCCAT 120  
Qy 121 TCCTTGACCGGCTTGGCCGAGACCAAGAGTCCCTAAAAGGAAGAGGTAGACACTCTTGTC 180  
Db 121 TCCTTGACCGGCTTGGCCGAGACCAAGAGTCCCTAAAAGGAAGAGGTAGACACTCTTGTC 180  
Qy 181 TGGACATCGAAACAGCCACTCGTGCAGGAAAGACAGATAGTGGAGCAGATTCCTGGAAGAG 240  
Db 181 TGGACATCGAAACAGCCACTCGTGCAGGAAAGACAGATAGTGGAGCAGATTCCTGGAAGAG 240  
Qy 241 AATCAGATGAGGCACTTAAATATGATGCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAAAGTAA 300  
Db 241 AATCAGATGAGGCACTTAAATATGATGCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAAAGTAA 300  
Qy 301 ACATGACTCTTATGATGATGCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAAAGTAA 360  
Db 301 ACATGACTCTTATGATGATGCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAAAGTAA 360  
Qy 361 CAGGCTCCCTATGATTAAGATGAGCAGCAGCAATCATGATAAGAACTCATACTTAAAG 420  
Db 361 CAGGCTCCCTATGATTAAGATGAGCAGCAGCAATCATGATAAGAACTCATACTTAAAG 420  
Qy 421 CAACTTTAGTGTGATTTTCCAAAGGCTGGAGACACTTAATGATGATGATGATGATG 480  
Db 421 CAACTTTAGTGTGATTTTCCAAAGGCTGGAGACACTTAATGATGATGATGATGATG 480  
Qy 481 AAGAAGGAGGCTGGTGGCGAAATTCACATTCGCTTCTTCCAGGACATTAATG 540  
Db 481 AAGAAGGAGGCTGGTGGCGAAATTCACATTCGCTTCTTCCAGGACATTAATG 540  
Qy 541 AGGATGTCAAAATGCAATTTGGGGTCTCATCGGAGGACTTAATGATGATGATGATG 600  
Db 541 AGGATGTCAAAATGCAATTTGGGGTCTCATCGGAGGACTTAATGATGATGATGATG 600  
Qy 601 TTAGAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGGAGTCAATGATGATGATG 660  
Db 601 TTAGAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGGAGTCAATGATGATGATG 660  
Qy 661 CTTCAATTCCTCCAAAGCAGAAACGAAATGAGAGAACTTAATGATGATGATGATG 720  
Db 661 CTTCAATTCCTCCAAAGCAGAAACGAAATGAGAGAACTTAATGATGATGATGATG 720  
Qy 721 GAAATAGATGTTGATTTGAAGAGAGTGGCAGACATAGATTTGAAATATACAGAAATAG 780  
Db 721 GAAATAGATGTTGATTTGAAGAGAGTGGCAGACATAGATTTGAAATATACAGAAATAG 780  
Qy 781 GAAACAATACATTTATGCAAGCCTTACAACTTATGCTTGAAGTAGAACAAGAGATAAGA 840  
Db 781 GAAACAATACATTTATGCAAGCCTTACAACTTATGCTTGAAGTAGAACAAGAGATAAGA 840  
Qy 841 ACTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTA 888  
Db 841 ACTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTA 888

RESULT 3

US-10-181-585B-39  
; Sequence 39, Application US/10181585B  
; Publication No. US20050175985A1  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System  
; APPLICANT: of Higher Education  
; APPLICANT: Dowling, Patricia W.



Db	421	CAAACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCG	480
Qy	481	AAGAAGGAGCAGTGGTTGGCGAAATTTTCCATTTGCCCTTCTTCCAGGACATATAATG	540
Db	481	AAGAAGGAGCAGTGGTTGGCGAAATTTTCCATTTGCCCTTCTTCCAGGACATATAATG	540
Qy	541	AGGATGTCAAAATGCAATTTGGGGTCTCATCGGAGACTTAAATGGAATGATAATACGG	600
Db	541	AGGATGTCAAAATGCAATTTGGGGTCTCATCGGAGACTTAAATGGAATGATAATACGG	600
Qy	601	TTAGATCTCTGAACTCTACAGAGATTGGCTTGGAGAGCAGTCAATGAGAAATGGGAGAC	660
Db	601	TTAGATCTCTGAACTCTACAGAGATTGGCTTGGAGAGCAGTCAATGAGAAATGGGAGAC	660
Qy	661	CTTCATTCCTCRAAGCAGAACGAAATGGAGAGCAATTTGAGCCAGAGTTTGA	720
Db	661	CTTCATTCCTCRAAGCAGAACGAAATGGAGAGCAATTTGAGCCAGAGTTTGA	720
Qy	721	GAAATAGATGGTTGATGAAAGTGGAGCAGTATGAAATGAAATACGAAATAGTTT	780
Db	721	GAAATAGATGGTTGATGAAAGTGGAGCAGTATGAAATGAAATACGAAATAGTTT	780
Qy	781	GACAAATACATTTATGCAAGCCTTACAACTATTGCTTGAAGTACAGACAGATAAGA	840
Db	781	GACAAATACATTTATGCAAGCCTTACAACTATTGCTTGAAGTACAGACAGATAAGA	840
Qy	841	ACTTCTCGTTTCAGCTATTATGATAAATAACACCCCTGTTCTA	888
Db	841	ACTTCTCGTTTCAGCTATTATGATAAATAACACCCCTGTTCTA	888
RESULT 5			
US-10-734-373-50			
; Sequence 50, Application US/10734373			
; Publication No. US20040137015A1			
; GENERAL INFORMATION:			
; APPLICANT: Dowling, Patricia W.			
; APPLICANT: Youngner, Julius S.			
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES			
; FILE REFERENCE: EQ-1-C2-1			
; CURRENT APPLICATION NUMBER: US/10734, 373			
; PRIOR FILING DATE: 2003-12-12			
; PRIOR APPLICATION NUMBER: PCT/US99/18583			
; PRIOR FILING DATE: 1999-08-12			
; PRIOR APPLICATION NUMBER: 09/133,921			
; PRIOR FILING DATE: 1998-08-13			
; NUMBER OF SEQ ID NOS: 108			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 50			
; LENGTH: 891			
; TYPE: DNA			
; ORGANISM: Equine influenza virus H3N8			
; FEATURE: CDS			
; NAME/KEY: (27) - (716)			
; OTHER INFORMATION:			
US-10-734-373-50			
Query Match			
Best Local Similarity 99.8%; Score 886.4; DB 7; Length 891;			
Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	1	ACCAAGAGCGGTGACAAACATATGATTCGAACACTGTCTCAAGCTTTCAGGTAG	60
Db	1	ACCAAGAGCGGTGACAAACATATGATTCGAACACTGTCTCAAGCTTTCAGGTAG	60
Qy	61	ACTGTTTCTTTGGCATGTCGCCAAACGATTTGCAGACCAAGACTGGGTGATGCCCAT	120
Db	61	ACTGTTTCTTTGGCATGTCGCCAAACGATTTGCAGACCAAGACTGGGTGATGCCCAT	120
Qy	121	TCCTTGACCGGCTTCGCCGAGACCGAAGATCCCTTAAAGAGAGGTAGCACTCTTGGTC	180
Db	121	TCCTTGACCGGCTTCGCCGAGACCGAAGATCCCTTAAAGAGAGGTAGCACTCTTGGTC	180

Qy	181	TGCAATCGAAACAGCCACTCGTGCAGAAAGCAGATAGTGGAGCAGATTCTTGAAGAGG	240
Db	181	TGCAATCGAAACAGCCACTCGTGCAGAAAGCAGATAGTGGAGCAGATTCTTGAAGAGG	240
Qy	241	AATCAGATGAGGCACTTAAATGACCATTTGCTCTGTTCTGCTTCCAGCTACTTAACTG	300
Db	241	AATCAGATGAGGCACTTAAATGACCATTTGCTCTGTTCTGCTTCCAGCTACTTAACTG	300
Qy	301	ACATGACTCTGATGAGATGTCAGAGAGCTGGTTCATGCTCATGCCCAAGCAGAAAGTAA	360
Db	301	ACATGACTCTGATGAGATGTCAGAGAGCTGGTTCATGCTCATGCCCAAGCAGAAAGTAA	360
Qy	361	CAGGCTCCCTATGATTAAGATGGACCGGCAATCATGGATAAGAAACATCATCTTAAAG	420
Db	361	CAGGCTCCCTATGATTAAGATGGACCGGCAATCATGGATAAGAAACATCATCTTAAAG	420
Qy	421	CAAACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCG	480
Db	421	CAAACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCG	480
Qy	481	AAGAAGGAGCAGTGGTTGGCGAAATTTCCACCATTTGCCCTTCTTCCAGGACATATAATG	540
Db	481	AAGAAGGAGCAGTGGTTGGCGAAATTTCCACCATTTGCCCTTCTTCCAGGACATATAATG	540
Qy	541	AGGATGTCAAAATGCAATTTGGGGTCTCATCGGAGACTTAAATGGAATGATAATACGG	600
Db	541	AGGATGTCAAAATGCAATTTGGGGTCTCATCGGAGACTTAAATGGAATGATAATACGG	600
Qy	601	TTAGATCTCTGAACTCTACAGAGATTGGCTTGGAGAGCAGTCAATGAGAAATGGGAGAC	660
Db	601	TTAGATCTCTGAACTCTACAGAGATTGGCTTGGAGAGCAGTCAATGAGAAATGGGAGAC	660
Qy	661	CTTCATTCCTCRAAGCAGAACGAAATGGAGAGCAATTTGAGCCAGAGTTTGA	720
Db	661	CTTCATTCCTCRAAGCAGAACGAAATGGAGAGCAATTTGAGCCAGAGTTTGA	720
Qy	721	GAAATAGATGGTTGATGAAAGTGGAGCAGTATGAAATGAAATACGAAATAGTTT	780
Db	721	GAAATAGATGGTTGATGAAAGTGGAGCAGTATGAAATGAAATACGAAATAGTTT	780
Qy	781	GACAAATACATTTATGCAAGCCTTACAACTATTGCTTGAAGTACAGACAGATAAGA	840
Db	781	GACAAATACATTTATGCAAGCCTTACAACTATTGCTTGAAGTACAGACAGATAAGA	840
Qy	841	ACTTCTCGTTTCAGCTATTATGATAAATAACACCCCTGTTCTA	888
Db	841	ACTTCTCGTTTCAGCTATTATGATAAATAACACCCCTGTTCTA	888
RESULT 6			
US-10-181-585B-32			
; Sequence 32, Application US/10181585B			
; Publication No. US20050175985A1			
; GENERAL INFORMATION:			
; APPLICANT: The University of Pittsburgh - of the Commonwealth System			
; APPLICANT: of Higher Education			
; APPLICANT: Dowling, Patricia W.			
; APPLICANT: Youngner, Julius S.			
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES			
; FILE REFERENCE: EQ-1-C3-PUS			
; CURRENT APPLICATION NUMBER: US/10/181.585B			
; PRIOR FILING DATE: 2003-12-08			
; PRIOR APPLICATION NUMBER: PCT/US01/05048			
; PRIOR FILING DATE: 2001-02-16			
; PRIOR APPLICATION NUMBER: 09/506,286			
; PRIOR FILING DATE: 2000-02-16			
; NUMBER OF SEQ ID NOS: 130			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 32			
; LENGTH: 891			
; TYPE: DNA			
; ORGANISM: Equine influenza virus H3N8			

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FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)...(716)
US-10-181-585B-32

Query Match      99.8%; Score 886.4; DB 9; Length 891;
Best Local Similarity 99.9%; Pred. No. 9e-232;
Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCAAGCAGGGTGACAAAACATAATGGATTCACACACTGTGTCAAGCTTTTCAGTAG 60
DB 1 AGCAAGCAGGGTGACAAAACATAATGGATTCACACACTGTGTCAAGCTTTTCAGTAG 60
QY 61 ACTGTTTCTTTGGCATGTCCGCAACAGATTTGCAGACCAAGAACTGGGTGATGCCCAT 120
DB 61 ACTGTTTCTTTGGCATGTCCGCAACAGATTTGCAGACCAAGAACTGGGTGATGCCCAT 120
QY 121 TCCTTGACCGGCTTCGCGAGAGACCAAGTCCCTAAAAGGAAGAGTAGCACTCTTGTC 180
DB 121 TCCTTGACCGGCTTCGCGAGAGACCAAGTCCCTAAAAGGAAGAGTAGCACTCTTGTC 180
QY 181 TGGACATCGAACAGCCACTCGTGAGGAAGACAGATAGTGAGCAGATTTGGAGAGG 240
DB 181 TGGACATCGAACAGCCACTCGTGAGGAAGACAGATAGTGAGCAGATTTGGAGAGG 240
QY 241 AATCAGATGAGGCACTTAAATGACCAATTCCTCTGTCTCTTCCAGCTACTTAACTG 300
DB 241 AATCAGATGAGGCACTTAAATGACCAATTCCTGTCTCTTCCAGCTACTTAACTG 300
QY 301 ACATGACTCTTGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAAAGTAA 360
DB 301 ACATGACTCTTGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAAAGTAA 360
QY 361 CAGGCTCCCTATGATTAAGAAATGACAGCAATCATGGAATGAACATCATCTTAAAG 420
DB 361 CAGGCTCCCTATGATTAAGAAATGACAGCAATCATGGAATGAACATCATCTTAAAG 420
QY 421 CAAACTTTAGTGTGATTTTGGAGAGGCTGGAGACCACTAATCTTCTAGAGCTTCACCG 480
DB 421 CAAACTTTAGTGTGATTTTGGAGAGGCTGGAGACCACTAATCTTCTAGAGCTTCACCG 480
QY 481 AGAAGAGAGAGCTGTGGGCAAAATTTCACTATGCTCTCTTCCAGCAATCTAATG 540
DB 481 AGAAGAGAGAGCTGTGGGCAAAATTTCACTATGCTCTCTTCCAGCAATCTAATG 540
QY 541 AGGATGTCAAAAATGCAATTTGGGCTCCTCATCGGAGGACTTAAATGGAATGATTAACGG 600
DB 541 AGGATGTCAAAAATGCAATTTGGGCTCCTCATCGGAGGACTTAAATGGAATGATTAACGG 600
QY 601 TTAGATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCAATGGAATGGAGAC 660
DB 601 TTAGATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCAATGGAATGGAGAC 660
QY 661 CTTCTATTCCTCCAAAGCAGAAAGATGGAGAGCAATTTGAGCCAGAGTTTGA 720
DB 661 CTTCTATTCCTCCAAAGCAGAAAGATGGAGAGCAATTTGAGCCAGAGTTTGA 720
QY 721 GAAATGAAGTGGTGTGATTAAGAGTGGAGCATGATGATGAAATGCAAAATGAGTTT 780
DB 721 GAAATGAAGTGGTGTGATTAAGAGTGGAGCATGATGATGAAATGCAAAATGAGTTT 780
QY 781 GAACAAAATGAATTTATGCAAGCTTTACAACTATTGCTTGAAGTAGAACAAGAGATAA 840
DB 781 GAACAAAATGAATTTATGCAAGCTTTACAACTATTGCTTGAAGTAGAACAAGAGATAA 840
QY 841 ACTTTCTGTTTCAGCTTATTTAATGATAAAACACCCCTTGTCTTCTA 888
DB 841 ACTTTCTGTTTCAGCTTATTTAATGATAAAACACCCCTTGTCTTCTA 888
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RESULT 7  
US-10-065-133A-53

; Sequence 53, Application US/10065133A

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Publication No. US20030199074A1
GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Younger, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-53

Query Match      99.6%; Score 884.4; DB 6; Length 888;
Best Local Similarity 99.9%; Pred. No. 3.2e-231;
Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CAAAGCAGGGTGACAAAACATAATGGATTCACACACTGTGTCAAGCTTTTCAGTAG 62
DB 1 CAAAGCAGGGTGACAAAACATAATGGATTCACACACTGTGTCAAGCTTTTCAGTAG 60
QY 63 TGTGTTTCTTTGGCATGTCCGCAACAGATTTGCAGACCAAGAACTGGGTGATGCCCATTC 122
DB 61 TGTGTTTCTTTGGCATGTCCGCAACAGATTTGCAGACCAAGAACTGGGTGATGCCCATTC 120
QY 123 CTTGACCGGCTTCGCGAGAGACCAAGTCCCTAAAAGGAAGAGTAGCACTCTTGCTG 182
DB 121 CTTGACCGGCTTCGCGAGAGACCAAGTCCCTAAAAGGAAGAGTAGCACTCTTGCTG 180
QY 183 GACATCGAAACAGCACTCTGTGAGGAAGAGATAGTGAGGAGATTTGGAAGAGAA 242
DB 181 GACATCGAAACAGCACTCTGTGAGGAAGAGATAGTGAGGAGATTTGGAAGAGAA 240
QY 243 TCAGATGAGGCACTTAAATGACCAATTCGCTCTGTCTCTGCTTCAAGCTTAACTGAC 302
DB 241 TCAGATGAGGCACTTAAATGACCAATTCGCTCTGTCTCTGCTTCAAGCTTAACTGAC 300
QY 303 ATGACTCTTTGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAAAGTAA 362
DB 301 ATGACTCTTTGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAAAGTAA 360
QY 363 GGCTCCCTATGTATAAGAAATGGACCAAGCAATCATGATTAAGAAACATCATCTTAAAGCA 422
DB 361 GGCTCCCTATGTATAAGAAATGGACCAAGCAATCATGATTAAGAAACATCATCTTAAAGCA 420
QY 423 AACTTTAGTGTGATTTTGGAGAGCTGGAGACCACTAATCTACTTAGAGCTTTACCGAA 482
DB 421 AACTTTAGTGTGATTTTGGAGAGCTGGAGACCACTAATCTACTTAGAGCTTTACCGAA 480
QY 483 GAAGGAGAGCTGTGGGCAAAATTTCACTTGGCTTCTTCTTCCAGGACATCTAATGAG 542
DB 481 GAAGGAGAGCTGTGGGCAAAATTTCACTTGGCTTCTTCTTCCAGGACATCTAATGAG 540
QY 543 GATGTCCAAAATGCAATTTGGGGTCCCTCATCGGAGGACTTAAATGGAATGATTAATACGGTT 602
DB 541 GATGTCCAAAATGCAATTTGGGGTCCCTCATCGGAGGACTTAAATGGAATGATTAATACGGTT 600
QY 603 AGAATCTCTGAACTCTACAGATTTCCGTTTGGAGAGCAGTCACTAGAAATGSGAGACT 662
DB 601 AGAATCTCTGAACTCTACAGATTTCCGTTTGGAGAGCAGTCACTAGAAATGSGAGACT 660
QY 663 TCATTCCTCCAAAGCAGAAACGAAATGGAAGAGCAATTTGAGCAGAGCTTTGAGA 722
DB 661 TCATTCCTCCAAAGCAGAAACGAAATGGAAGAGCAATTTGAGCAGAGCTTTGAGA 720
QY 723 AATAAGATGGTTGATTGAAGAGAGTGGCAATAGATTGGAATAATACAGAAATAGTTTGA 782
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Wed Mar 8 09:11:18 2006

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Db 721 AATAAGATGGTGTGATGAGAGAGTGGAGATGATGAAATATACAGAAATAGTTTGA 780
Qy 783 ACAATATACATTTATGCGAGGCTTACACTATTGCTTGAAGTAGAACAAGAGATAAGAAC 842
Db 781 ACAATATACATTTATGCGAGGCTTACACTATTGCTTGAAGTAGAACAAGAGATAAGAAC 840
Qy 843 TTTCTCGTTTCAGCTTATTTATGATATATAAACAACCCCTGTTTCTA 888
Db 841 TTTCTCGTTTCAGCTTATTTATGATATATAAACAACCCCTGTTTCTA 886

RESULT 8
US-10-734-373-53
; Sequence 53, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-734-373-53

Query Match 99.6%; Score 884.4; DB 7; Length 888;
Best Local Similarity 99.9%; Pred. No. 3.2e-231;
Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAAAGCAGGGTGACAAAAACATAATGGATTCCAACTGTGTCAAGCTTTTCAGGTAGAC 62
Db 1 CAAAGCAGGGTGACAAAAACATAATGGATTCCAACTGTGTCAAGCTTTTCAGGTAGAC 60
Qy 63 TGTGTTCTTTGGCATGTCGCAACGATTTGCGAGACCAAGACTGGGTGATGCCCATTC 122
Db 61 TGTGTTCTTTGGCATGTCGCAACGATTTGCGAGACCAAGACTGGGTGATGCCCATTC 120
Qy 123 CTTGACCGGCTTCGCGAGACCAAGATCCCTTAAAGAGAGAGTAGTGTGCTTCAAGCTTTTCAGGTAGAC 182
Db 121 CTTGACCGGCTTCGCGAGACCAAGATCCCTTAAAGAGAGAGTAGTGTGCTTCAAGCTTTTCAGGTAGAC 180
Qy 183 GACATCGAAACAGCCACTTCTGTCAGAGACAGAGTAGTGTGAGAGAGAGAA 242
Db 181 GACATCGAAACAGCCACTTCTGTCAGAGACAGAGTAGTGTGAGAGAGAGAA 240
Qy 243 TCAGATGAGGCACTTAAATGACATTCCTTCTGCTTCAAGCTTTTCAGGTAGAC 302
Db 241 TCAGATGAGGCACTTAAATGACATTCCTTCTGCTTCAAGCTTTTCAGGTAGAC 300
Qy 303 ATGACTCTTGTATGATGTCAAGAGACTGGTTTATGCTCATGCCCAAGCAAGAGTAACA 362
Db 301 ATGACTCTTGTATGATGTCAAGAGACTGGTTTATGCTCATGCCCAAGCAAGAGTAACA 360
Qy 363 GGTCTCTCTATGATTAAGAATGGACCAAGCAATCATGTTAAGAAACATCATCTTTAAGCA 422
Db 361 GGTCTCTCTATGATTAAGAATGGACCAAGCAATCATGTTAAGAAACATCATCTTTAAGCA 420
Qy 423 AACTTTAGTGTGATTTTTCGAAAGGCTGGAGACACTAATATCTTTAGAGCCTTCACCGAA 482
Db 421 AACTTTAGTGTGATTTTTCGAAAGGCTGGAGACACTAATATCTTTAGAGCCTTCACCGAA 480
Qy 483 GAAGGAGCAGTGTGGCGAAATTTCCACATTTGCTTCTTCCAGGACATCATTAATGAG 542
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Db 481 GAAGGAGCAGTGTGGCGAAATTTCCACATTTGCTTCTTCCAGGACATCATTAATGAG 540
Qy 543 GATGTCAAAATGCAATTTGGGTCTCTATCGAGGACTTAAATGAATGAATATACGTT 602
Db 541 GATGTCAAAATGCAATTTGGGTCTCTATCGAGGACTTAAATGAATGAATATACGTT 600
Qy 603 AGAATCTCTGAACTCTACAGAGATTCGTTTGGAGAGCAGTCATGAGAAATGGAGACCT 662
Db 601 AGAATCTCTGAACTCTACAGAGATTCGTTTGGAGAGCAGTCATGAGAAATGGAGACCT 660
Qy 663 TCAATCCCTCCAAAGCAGAAACGAAATATGAGAGAACTTTGAGCCAGAGTTTGA 722
Db 661 TCAATCCCTCCAAAGCAGAAACGAAATATGAGAGAACTTTGAGCCAGAGTTTGA 720
Qy 723 AATAAGATGGTGTGATGAGAGAGTGGACATAGATTGAAAAATACAGAAATAGTTTGA 782
Db 721 AATAAGATGGTGTGATGAGAGAGTGGACATAGATTGAAAAATACAGAAATAGTTTGA 780
Qy 783 ACAATATACATTTATGCAAGCCTTACACTATTGCTTGAAGTAGAACAAGAGATAAGAAC 842
Db 781 ACAATATACATTTATGCAAGCCTTACACTATTGCTTGAAGTAGAACAAGAGATAAGAAC 840
Qy 843 TTTCTCGTTTCAGCTTATTTATGATATATAAACAACCCCTGTTTCTA 888
Db 841 TTTCTCGTTTCAGCTTATTTATGATATATAAACAACCCCTGTTTCTA 886

RESULT 9
US-10-181-585B-35
; Sequence 35, Application US/10181585B
; Publication No. US20050175985A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C3-PUS
; CURRENT APPLICATION NUMBER: US/10/181,585B
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: PCT/US01/05048
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/506,286
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-181-585B-35

Query Match 99.6%; Score 884.4; DB 9; Length 888;
Best Local Similarity 99.9%; Pred. No. 3.2e-231;
Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAAAGCAGGGTGACAAAAACATAATGGATTCCAACTGTGTCAAGCTTTTCAGGTAGAC 62
Db 1 CAAAGCAGGGTGACAAAAACATAATGGATTCCAACTGTGTCAAGCTTTTCAGGTAGAC 60
Qy 63 TGTGTTCTTTGGCATGTCGCAACGATTTGCGAGACCAAGACTGGGTGATGCCCATTC 122
Db 61 TGTGTTCTTTGGCATGTCGCAACGATTTGCGAGACCAAGACTGGGTGATGCCCATTC 120
Qy 123 CTTGACCGGCTTCGCGAGACCAAGATCCCTTAAAGAGAGAGTAGTGTGCTTCAAGCTTTTCAGGTAGAC 182
Db 121 CTTGACCGGCTTCGCGAGACCAAGATCCCTTAAAGAGAGAGTAGTGTGCTTCAAGCTTTTCAGGTAGAC 180
Qy 183 GACATCGAAACAGCCACTTCTGTCAGAGACAGAGTAGTGTGAGAGAGAGAA 242
Db 181 GACATCGAAACAGCCACTTCTGTCAGAGACAGAGTAGTGTGAGAGAGAGAA 240
Qy 243 TCAGATGAGGCACTTAAATGACATTCCTTCTGCTTCAAGCTTTTCAGGTAGAC 302
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Db 241 TCAGATGAGGACATTAAATGACCATTCCTGCTGCTTTCAGCTTACTTAACTGAC 300
Qy 303 ATGACTCTTGATGAGATGTCAGAGACTGGTTTCATGCTCATGCTGCCAAGCAGAAAGTAACA 362
Db 301 ATGACTCTTGATGAGATGTCAGAGACTGGTTTCATGCTCATGCTGCCAAGCAGAAAGTAACA 360
Qy 363 GGTCTCCCTATGTAAGAATGGACAGGCAATCATGATAAGAAATCATATCTTAAAGCA 422
Db 361 GGTCTCCCTATGTAAGAATGGACAGGCAATCATGATAAGAAATCATATCTTAAAGCA 420
Qy 423 AACTTTAGTGTGATTTTCGAAAGCTTGGAGACACTAATATCTTCTAGAGCTTCCACCGNA 482
Db 421 AACTTTAGTGTGATTTTCGAAAGCTTGGAGACACTAATATCTTCTAGAGCTTCCACCGNA 480
Qy 483 GAAGGAGCAGTCGTTGGGAAATTTCCACCATTCGCTTCTTCCAGGACACTAATATGAG 542
Db 481 GAAGGAGCAGTCGTTGGGAAATTTCCACCATTCGCTTCTTCCAGGACACTAATATGAG 540
Qy 543 GATGCAAAATGCAATGGGTCCTCATCGAGAGCTTAAATGGAAATGATATACGGTT 602
Db 541 GATGCAAAATGCAATGGGTCCTCATCGAGAGCTTAAATGGAAATGATATACGGTT 600
Qy 603 AGAATCTGAAACTCTACAGAGATTCGTTGGAGAGAGCTCATGAGAAATGGAGACCT 662
Db 601 AGAATCTGAAACTCTACAGAGATTCGTTGGAGAGAGCTCATGAGAAATGGAGACCT 660
Qy 663 TCATTCCCTCCAAAGCAGAAACGAAATGGAGAGAAATTCGAGCCAGAAAGTTGAAGA 722
Db 661 TCATTCCCTCCAAAGCAGAAACGAAATGGAGAGAAATTCGAGCCAGAAAGTTGAAGA 720
Qy 723 AATAAGATGGTTGATTCGAAGAGTCGACATAGATTCGAAATACAGAAATAGTTTGA 782
Db 721 AATAAGATGGTTGATTCGAAGAGTCGACATAGATTCGAAATACAGAAATAGTTTGA 780
Qy 783 ACAATAACATTTATGCAAGCTTACCACTTTCCTTGAAGTAGACAGAGATAAGAAC 842
Db 781 ACAATAACATTTATGCAAGCTTACCACTTTCCTTGAAGTAGACAGAGATAAGAAC 840
Qy 843 TTTCGCTTCAGCTTATTAATGATAAAGACCCCTGTTCTTA 888
Db 841 TTTCGCTTCAGCTTATTAATGATAAAGACCCCTGTTCTTA 886
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## RESULT 10

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US-10-855-875-6
; Sequence 6, Application US/10855875
; Publication No. US2005000349A1
; GENERAL INFORMATION:
; APPLICANT: Kawaoka, Yoshihiro
; TITLE OF INVENTION: High Titer Recombinant Influenza Viruses for Vaccines and Gene Th
; FILE REFERENCE: 800.038U81
; CURRENT APPLICATION NUMBER: US/10/855,875
; PRIOR FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US 60/473,798
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 890
; TYPE: DNA
; ORGANISM: Influenza virus
US-10-855-875-6
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Query Match 83.6%; Score 742.4; DB 8; Length 890;
Best Local Similarity 89.8%; Pred. No. 2.4e-182; Mismatches 91; Indels 0; Gaps 0;
Matches 797; Conservative 0;

Qy 1 AGCAAAAGCAGGTCACAAAACATTAATGGATTCACACTGTGTCAAGCTTCAGGTAG 60
Db 1 AGCAAAAGCAGGTCACAAAACATTAATGGATTCACAACTGTGTCAAGCTTCAGGTAG 60
Qy 61 ACTGTTTCTTGGCATGTCGCCAAACGATTTGCGAGACCAAGAACTGGGTGATGCCCCAT 120
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Db 61 ATTGCTTCTTTGGCATGTCGCCAAACGATTTGCGAGACCAAGAACTAGCGATGCCCAT 120
Qy 121 TCCTTGACCGGCTTCGCCGAGACAGAAAGTCCCTAAAAAGGAAGAGGTAGCACTCTTGCTC 180
Db 121 TCCTTGATCGGCTTCGCCGAGATCAGAAATCCCTAAGAGGAAGGGGAGTACTCTCGGTC 180
Qy 181 TGACATCGAAACAGCCACTCGTGCAGGAAGACATAGTGGAGCAGATTTCTGGAGAGG 240
Db 181 TGACATCAAGACAGCCACAGCTGCTGGAAACGACATAGTGGAGCGGATTCGAAAGAG 240
Qy 241 ANTACATGAGCAGCATTAAATGACCATTCGCTCTGCTTCCCTGCTCAGCTTAACTG 300
Db 241 ANTCCGATGAGCAGCATTAAATGACCATTCGCTCTGCTGCTGCTGCTGCTTAACTG 300
Qy 301 ACATGACTCTTGATGAGATGTCAGAGACTGGTTTCATGCTCATGCTCATGCCAGCAAGATAA 360
Db 301 ACATGACTCTTGAGGAATGTCAGGAGCTGGTTCATGCTCATGCTCATGCCAGCAAGATAA 360
Qy 361 CAGGCTCCCTATGTAAGAATGGACAGGCAATCATGGAATAGACATCATCTTAAAG 420
Db 361 CAGGCTCCCTATGTAAGAATGGACAGGCAATCATGGAATAGACATCATCTTAAAG 420
Qy 421 CAACTTTAGTGTGATTTTCGAAAGCTTCGAGACACTAATACTACTAGAGCTTCAACG 480
Db 421 CAACTTTAGTGTGATTTTCGAAAGCTTCGAGACACTAATACTACTAGAGCTTCAACG 480
Qy 481 AAGAGGAGCAGCTCGTGGGAAATTTCCACCATTCGCTTCTCTCCAGGACATATAATG 540
Db 481 AAGAGGAGCAATTTGCGGCAATTTCCACCATTCGCTTCTCTCCAGGACATATACTGCTG 540
Qy 541 AGGATGTCAAAATGCAATTTGGGCTCCTCATCGAGGACTTTAAATGGAATGATAATACGG 600
Db 541 AGGATGTCAAAATGCAATTTGGGCTCCTCATCGAGGACTTTGGAATGGAATGATAACAG 600
Qy 601 TTAGATCTCTCAAACTCTACAGAGATTCGTTGGAGAGCAGCTCATGAGATGGAGAC 660
Db 601 TTCGAGTCTCTGAACTCTACAGAGATTCGTTGGAGAGCAGCTCATGAGATGGAGAC 660
Qy 661 CTTTCATCCCTCCAAAGCAGAAATGGAGAGCAATTTGAGAGCAATTTGAGAGCTTCA 720
Db 661 CTTTCATCCCTCCAAAGCAGAAATGGAGAGCAATTTGAGAGCAATTTGAGAGCTTCA 720
Qy 721 GAAATAGATGTTGATTTGAGAGAGTGGCAGATAGATGAAATACAGAAATAGTTTT 780
Db 721 GAAATAGATGTTGATTTGAGAGAGTGGCAGATAGATGAAATACAGAAATAGTTTT 780
Qy 781 GAACAAAATACATTTATGCAAGCTTTCACAACTTATGCTTGAAGTAGAACAAGAGATAAGA 840
Db 781 GAGCAAAATACATTTATGCAAGCTTTCACATCTTATGCTTGAAGTAGGAGCAAGAGATAAGA 840
Qy 841 ACTTTCCTGTTTCAGCTTATTTAATGATAAAGACCCCTGTTCTTA 888
Db 841 ACTTTCCTGTTTCAGCTTATTTAATGATAAAGACCCCTGTTCTTA 888
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## RESULT 11

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US-10-381-530-8
; Sequence 8, Application US/10381530
; Publication No. US20040137013A1
; GENERAL INFORMATION:
; APPLICANT: KATINGER, Hermann
; APPLICANT: EGOROV, Andre
; APPLICANT: FERKO, Boris
; APPLICANT: ROMANOVA, Julia
; APPLICANT: KATINGER, Dietmar
; TITLE OF INVENTION: LIVE VACCINE AND METHOD OF MANUFACTURE
; FILE REFERENCE: P/167-134
; CURRENT APPLICATION NUMBER: US/10/381,530
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: PCT/EP01/11087
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 00120896.6
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; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 890
; TYPE: DNA
; ORGANISM: Influenza virus A/Singapore/1/57/ca
US-10-381-530-8

Query Match      83.1%; Score 737.6; DB 7; Length 890;
Best Local Similarity 89.4%; Pred. No. 4.9e-191; Indels 0; Gaps 0;
Matches 794; Conservative 0; Mismatches 94;

QY 1 AGCAAAAGCAGGGTGACAAAACATATGGATTCCACACTGTCACAGCTTCCAGTAG 60
Db 1 AGCAAAAGCAGGGTGACAAAACATATGGATTCCACACTGTCACAGCTTCCAGTAG 60
QY 61 ACTGTTTCTTTGGGATGTCGGCAAAACGATTTGCGAGACCAAGACTGGGTATGCCCAT 120
Db 61 ATTGCTTCTTTGGCATGTCGGCAAAACGATTTGCGAGACCAAGACTGGGTATGCCCAT 120
QY 121 TCCTTGACCGGCTTCGCGGAGACCAAGATCCCTTAAAGAGAGAGTAGACTCTTGGTC 180
Db 121 TCCTTGATCGGCTTCGCGGAGATCAGAGTCCCTTAAAGGAGAGAGGACACTCTCGGTC 180
QY 181 TGACACATCGAAACAGCCACTGTCGAGGAAAGCAGATAGTGGAGCGAGATTCGAGAGG 240
Db 181 TGAACATCGAAACAGCCACCCTGTTGGAAAGCAGATAGTGGAGAGATTCGAAAGAG 240
QY 241 AATCAGATGAGGCACTTAAATAGCAATTCCTCTGTTTCTGCTTCAACGCTACTTAATCTG 300
Db 241 AATCCGATGAGGCACTTAAATAGCAATTCCTCTGTTTCTGCTTCAACGCTACTTAATCTG 300
QY 301 ACATGACTCTTATGAGATGTCAAGAGACTGGTTTCATGCTCATGCCCAAGCAGAAAGTAA 360
Db 301 ACATGACTTATGAGAAATGTCAAGGACTGGTTTCATGCTTAATGCCCAAGCAGAAAGTGT 360
QY 361 CAGGCTCCCTATGTATTAAGAAATGGACAGGCAATCATGATAAGAACTATCACTTAAAG 420
Db 361 CAGGCTCCCTTGTATFCAAGAAATGGACAGGCAATCATGATAAGAACTATCACTTAAAG 420
QY 421 CAATCTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATCTACTTATAGAGCTTTCACCG 480
Db 421 CGAATTTCACTGTGATTTTTCGACCGGCTAGAGACCTAATCTACTTATAGAGCTTTCACCG 480
QY 481 AAGAGGAGCAGTCGTTGGCGAAATTTTCACTTGGCTTCTCTTCCAGGACATCTAATG 540
Db 481 AAGAGGAGCAATTTGTCGGAATTTTCACTTGGCTTCTCTTCCAGGACATCTAATG 540
QY 541 AGGATGTCAAAATGCAATTTGGGTCCTCATCGAGGACTTAAATGGAATGATAACG 600
Db 541 AGGATGTCAAAATGCAATTTGGGTCCTCATCGAGGACTTGAATGGAATGATAACAG 600
QY 601 TTAGATCTCTGAACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGGAGAC 660
Db 601 TTCGAGTCTCTAAATCTCTACAGAGATTCGCTTGGAGAGCACTGAATGGAATGGAGAG 660
QY 661 CTTTCATCCCTCCAAAGCAGAAACGAAATGAGAGAACTTGGCCGCAAGTTTGAA 720
Db 661 CTTCCACTCACTCCAAACAGAAACGAAATGAGAGAACTTGGCCGCAAGTTTCGAA 720
QY 721 GAAATAAGATCGTTGATTCAGAGATTCGACATAGATGAAATAACAGAAATAGTTTTT 780
Db 721 GAAATAAGATCGCTGATTTGAGAGTGGAGACCAATTAATGAAATACAGAGATAGTTTT 780
QY 781 GAAACAAATAACATTTATGCAAGCTTACACTATTGCTTGAATGAGACAGAGATAAGA 840
Db 781 GAGCAAAATAACATTTATGCAAGCTTACAGCTGCTATTGAGAGTGGACAGAGATAAGA 840
QY 841 ACTTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTTCTTA 888
Db 841 ACTTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTTCTTA 888

RESULT 12
US-10-654-737-2
; Sequence 2, Application US/10654737
; Publication No. US20050054846A1
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital
; APPLICANT: Webster, Robert G
; APPLICANT: Webby, Richard J
; APPLICANT: Ozaki, Hiroichi
; TITLE OF INVENTION: Improved Method for Generating Influenza Viruses and Vaccines
; FILE REFERENCE: SJ-02-0016
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; TYPE: DNA
; ORGANISM: Influenza A virus
US-10-654-737-2

Query Match      78.0%; Score 692.8; DB 9; Length 824;
Best Local Similarity 90.0%; Pred. No. 8.6e-179; Indels 0; Gaps 0;
Matches 742; Conservative 0; Mismatches 82;

QY 22 ACATATATGATTTCCAAACACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCC 81
Db 1 ACATATATGATTTCCAAACACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCC 60
QY 82 GCAAACGATTTTCAGACCAAGAACTGGGTGATGCCCATTCCTTTGACCGGCTTTCGCCGAG 141
Db 61 GCBAACGATTTTCAGACCAAGAACTAGGTGATGCCCATTCCTTTGATCGGCTTTCGCCGAG 120
QY 142 ACCGAGATCCCTTAAAGGAAGAGTAGACACTCTTGTCTGACATCGAAACAGGCACATC 201
Db 121 ATCAGAACTCCCTTACAGAGAGAGGACGACACTCTCGGCTGAAACATCGAAACAGGCATCC 180
QY 202 GTGCAAGAGCAGATAGTGGAGCAGATTTCTGGAGAGGAATCAGATGAGGCACTTAAAA 261
Db 181 GTGCTGGAAAGCAATAGTGGAGCGGATTCGAGAGGAAGATCCGATGAGGCACTTAAAA 240
QY 262 TGAACATGCTCTGTTCTGCTTCACTTACTTACATGACATGACTCTTTGATGAGATGT 321
Db 241 TGACCTGGCTCTGCACTGCTTGGCTTCTTACTGACATGACTTATTGAGGAATGT 300
QY 322 CAAGGACTGGTTCTATGCTTCATGCCCAAGCAGAAAGTACAGGCTCCCTATGATATAAGAA 381
Db 301 CAAGGACTGGTTCTATGCTTCATGCCCAAGCAGAAAGTGGCAGGCCCTCTTTGTATCAGAA 360
QY 382 TGGACCAAGCAATCATGGAATAGAACATCATCTTAAAGCAACTTTAGTGTGATTTTCG 441
Db 361 TGGACCAAGCGATCATGGAATAGAGCATCATCTATGAAAGCACTTCASTGTGATTTTG 420
QY 442 AAAGCTGGAGACATAAATACTATTAGAGCTTCCCGAAGAGAGCAGTCTGGCG 501
Db 421 ACCGGCTGGAGACTTAAATATTACTTAAGGGCTTTTCCCGAGAGGAGCAATTTGGCG 480
QY 502 AAATTTCAACATTCGCTTCTTCTCCAGACATATAATAGAGATGCAAAATCGAATTCG 561
Db 481 AAATTTCAACATTCGCTTCTTCTCCAGACATATAATAGAGATGCAAAATCGAATTCG 540
QY 562 GGGTCTCATCGGAGGACTTAAATGGAATGATAACGTTAGATCTCTGAACTCTAC 621
Db 541 GGGTCTCATCGGAGGACTTGAATGGAATATAACAGTTCAGTCTCTAACTCTAC 600
QY 622 AGAGATTCGCTTGGAGAGCAGTCATGAGAAATGGGAGACCTTCATTCCTCCAAAGCAGA 681
Db 601 AGAGATTCGCTTGGAGAGCAGTAATGAGAAATGGGAGACCTTCACCTCACTCCAAAGCAGA 660
QY 682 AACGAAATGAGAGAGCAATTTGAGCCAGCAAGTTTGAAGAAATAGATGGTGTGATGAA 741
Db 661 AACGAAATGAGAGAGCAATTTAGGTGAGAGTATTGAGAAATAGATGGTGTGATGAA 720
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Db      481  TCACCAATTCCTCTCTCCAGGACATACATAATGAGATGTCAAAATGCAATGGGGTC 540
Qy      567  CTCATCGGAGGACTTAAATGGAATGATATACGGTTAGAAATCTCTGAAACTCTACAGAGA 626
Db      541  CTCATCGGAGGACTTAAATGGAATGATATACGGTTAGAAATCTCTGAAACTCTACAGAGA 600
Qy      627  TTCGCTTGGAGAGCAGTCATGAGATGGAGACCTTCATTCCCTCCAAAGCAGAAACGA 686
Db      601  TTCGCTTGGAGAGCAGTCATGAGATGGAGACCTTCATTCCCTCCAAAGCAGAAACGA 660
Qy      687  AAAATGGAGAGCAATTTGAGCCAGAGTT 716
Db      661  AAAATGGAGAGCAATTTGAGCCAGAGTT 690

RESULT 15
US-10-734-373-52
; Sequence 52, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-734-373-52
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Query Match      77.7%; Score 690; DB 7; Length 690;
Best Local Similarity 100.0%; Pred. No. 4.6e-178;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      27  ATGGATTCCAAACACTGTCTCAAGCTTTTCAGGTAGACTGTCTTTCTTTGGCATGTCCGCAA 86
Db      1  ATGGATTCCAAACACTGTCTCAAGCTTTTCAGGTAGACTGTCTTTCTTTGGCATGTCCGCAA 60
Qy      87  CGATTTTCAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCCGAGACCAG 146
Db      61  CGATTTTCAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCCGAGACCAG 120
Qy     147  AAGTCCCTAAAGAGAGGTAGCAGCTCTGGTCTGGACATCGAAACAGCAGCACTGTGCA 206
Db     121  AAGTCCCTAAAGAGAGGTAGCAGCTCTGGTCTGGACATCGAAACAGCAGCACTGTGCA 180
Qy     207  GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACC 266
Db     181  GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACC 240
Qy     267  ATTGCCTCTGTTCTCGCTTCAGCTACTTAATGACATGACTCTTTGATGAGATGTCAAGA 326
Db     241  ATTGCCTCTGTTCTCGCTTCAGCTACTTAATGACATGACTCTTTGATGAGATGTCAAGA 300
Qy     327  GACTGGTTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATAGAAATGGAC 386
Db     301  GACTGGTTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATAGAAATGGAC 360
Qy     387  CAGGCAATCATGATAGAAACATCATACTTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG 446
Db     361  CAGGCAATCATGATAGAAACATCATACTTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG 420
Qy     447  CTGGAGACACTAATACTACTTAGAGCCTTCACCGAAGAGGAGCAGTCTGTGGCGAAATT 506

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Job time : 927.202 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 01:03:53 ; Search time 416.426 Seconds  
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Title: US-10-734-373-57

Perfect score: 888

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Gapop 10.0 , Gapext 1.0

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Maximum Match 100%

Listing first 45 summaries

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- 12: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	41.2	4.6	218821	12	US-11-121-086-31
2	40.8	4.6	2295	8	US-10-750-185-31619
3	40.8	4.6	2295	8	US-10-750-623-31619
4	39.8	4.5	566	6	US-09-925-065A-553911
5	39.8	4.5	1524	6	US-09-925-065A-553280
6	39.2	4.4	626	6	US-09-925-065A-408866
7	39.2	4.4	1279	6	US-09-925-065A-92744
8	39.2	4.4	1279	6	US-09-925-065A-92745
9	39	4.4	584	6	US-09-925-065A-452283
10	38.8	4.4	483	6	US-09-925-065A-265276
11	38.8	4.4	528	6	US-09-925-065A-597659
12	38.4	4.3	549	6	US-09-925-065A-279044
13	38.4	4.3	549	6	US-09-925-065A-279045
14	38.4	4.3	623	6	US-09-925-065A-766520
15	38.4	4.3	631	6	US-09-925-065A-771317
16	38.2	4.3	575	6	US-09-925-065A-354936
17	38	4.3	281	6	US-09-925-065A-632446
C 18	38	4.3	2721	8	US-10-750-185-52450
C 19	38	4.3	2721	8	US-10-750-623-52450
20	37.8	4.3	474	6	US-09-925-065A-543248

C 21	37.8	4.3	617	6	US-09-925-065A-576543
22	37.8	4.3	700	6	US-09-925-065A-165231
C 23	37.6	4.2	537	6	US-09-925-065A-336212
C 24	37.6	4.2	537	6	US-09-925-065A-336213
C 25	37.6	4.2	682	5	US-09-978-360A-120
C 26	37.6	4.2	1263	8	US-10-527-500-14
C 27	37.6	4.2	121160	7	US-10-330-773-847
C 28	37.6	4.2	254396	7	US-10-330-773-534
C 29	37.4	4.2	635	6	US-09-925-065A-515303
C 30	37.4	4.2	1084	6	US-09-925-065A-704356
C 31	37.4	4.2	3850	6	US-09-925-065A-690067
C 32	37.2	4.2	242	6	US-09-925-065A-410546
C 33	37.2	4.2	530	6	US-09-925-065A-357347
C 34	37.2	4.2	110469	7	US-10-330-773-314
C 35	37	4.2	172649	12	US-11-121-086-36
C 36	36.8	4.1	578	6	US-09-925-065A-82370
C 37	36.8	4.1	622	6	US-09-925-065A-758895
C 38	36.8	4.1	623	6	US-09-925-065A-749905
C 39	36.8	4.1	676	6	US-09-925-065A-524064
C 40	36.8	4.1	1564	8	US-10-750-185-52400
41	36.8	4.1	1564	8	US-10-750-623-52400
C 42	36.8	4.1	2131	6	US-09-925-065A-74502
C 43	36.8	4.1	2131	6	US-09-925-065A-74503
C 44	36.8	4.1	2131	6	US-09-925-065A-74504
C 45	36.8	4.1	2131	6	US-09-925-065A-74505

#### ALIGNMENTS

RESULT 1  
US-11-121-086-31/c  
; Sequence 31, Application US/11121086  
; Publication No. US20050266459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; APPLICANT: NIELSEN, KIRSTEN V.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138 6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121,086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 31  
; LENGTH: 218821  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified base  
; LOCATION: (106949)..(106949)  
; OTHER INFORMATION: a, c, g, t, unknown or other  
; FEATURE:  
; NAME/KEY: modified base  
; LOCATION: (110322)..(110324)  
; OTHER INFORMATION: a, c, g, t, unknown or other  
; FEATURE:  
; NAME/KEY: modified base  
; LOCATION: (115133)..(115133)  
; OTHER INFORMATION: a, c, g, t, unknown or other  
; FEATURE:  
; NAME/KEY: modified base  
; LOCATION: (131300)..(131300)  
; OTHER INFORMATION: a, c, g, t, unknown or other  
; FEATURE:  
; NAME/KEY: modified base  
; LOCATION: (139059)..(139158)  
; OTHER INFORMATION: a, c, g, t, unknown or other  
; FEATURE:  
; NAME/KEY: modified base  
; LOCATION: (157740)..(157740)  
; OTHER INFORMATION: a, c, g, t, unknown or other

9

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; LOCATION: (200349) ..(200349)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (200351) ..(200351)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (212425) ..(212426)
; OTHER INFORMATION: a, c, g, t, unknown or other
US-11-121-086-31

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	Query Match	4.8%;	Score 41.2;	DB 12;	Length 21821;
	Best Local Similarity 53.0%;	Pred. No. 20;			
	Matches 88;	Conservative 0;	Mismatches 78;	Indels 0;	Gaps 0;
QY	657	AGACCTTCATTCCTCCAAAGCAGAAACGAAAAATGGAGAGAACAAATTGAGCCAGAAAGTT	716		
Db	125425	AAAAATACAAAACCAATAAGTAAAAAGAGAGAGAGAAAGACATATAAATTGAGAAATT	125366		
QY	717	TGAAGAAATAAGATGTGTTGTTGAAGAAAGTGCACATAGATTGAAAAATACAGAAAATAG	776		
Db	125365	TGATGTAAACATTCTGTGATGAAGGATGCAAAAACAAATGTTTAAAGGCAATAAATAG	125306		
QY	777	TTTTGAACAAATACATTTATTCGAGCCTTACACTATTGTCTGAA	822		
Db	125305	CCTTGGAGAGAGAAATTTCTCTGAAGTATTCAATAATTATTAGTCAA	125260		

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RESULT 2
US-10-750-185-31619
; Sequence 31619, Application US/10750185
; Publication NO. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31619
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-31619

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	Query Match	Score 40.8;	DB 8;	Length 2295;
	Best Local Similarity 49.5%;	Prod. No. 5;		
	Matches 105;	Conservative 0;	Mismatches 107;	Indels 0; Gaps 0;
QY	662	TTCAATTCCCTCAAAGCAGAAACGAAAAATGAGAGAGAAACAATTGAGCCGACAGATTGTGAAG	721	
DB	1191	TTCTTTCTCTGAAGATTTTGAAAGGTTTAAGTGAATTTGAGAAATTTGTATAACTATGTTTCATAA	1250	
QY	722	AAATAAGATGGTTTGATTCAGAGAGTCGCAATAGATTCGAAATAATCAGAAATAGCTTTTG	781	
DB	1251	AAATTAAAGATTGAGAAAAAATGTTTAACTGAACTAGAAACATAGAAAGTAAACACTT	1310	
QY	782	ACAAATATACATTTATGACGCCTTCAACTATTTCCTTGAAGTAGAACCAAGAGATAAGAA	841	
DB	1311	CAAAAATATATACCTTAATGTGCTCAACCAATTCAGTACTTTGTTTCATCTACTTCAAAGTGATAT	1370	
QY	842	CTTCTTCGTTTTCAGCTTATTTTAATGATAAAAA	873	

Db 1371 CTACTCTCTTTCTGTCGTTATGCTCATAAA 14002

RESULT 3

US-10-750-623-31619

; Sequence 31619, Application US/10750623

; Publication No. US20050287531A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFER

; FILE REFERENCE: MM100-1

; CURRENT APPLICATION NUMBER: US/10/750,623

; PRIOR FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 31619

; LENGTH: 2295

; TYPE: DNA

; ORGANISM: Bovine

US-10-750-623-31619

Query Match	4.6%	Score 40.8;	DB 8;	Length 2295;
Best Local Similarity	49.5%;	Prod. No. 5;		
Matches 105;	Conservative 0;	Mismatches 107;	Indels 0;	Gaps 0;
QY	662	TTCAATCCCTCAAAGCAGAAACGAAAAATGGAGAGAACAAATTGACGCGAAGTTTGAAG	721	
Db	1191	TTCTTTTCTCTGAAGATTGGAAGGTTAACTGAAATTTGAGAAATTTGATAACTATGTTTCATAA	1250	
QY	722	AAATAAGATGGTTGATTTGAAGAACTGCGACATAGATTGAAAAATACAGAAAAATAGTTTTG	781	
Db	1251	AAATTAAAGAAATTGAGAAAAAAATGTTTAACTGAAACTAGAACATAGAAAGTAAAGCACTT	1310	
QY	782	AACAAATAACATTTTATGCAAGCCCTTACAACACTATGCTTTGAAGTAGAACCAAGAGATAAGAA	841	
Db	1311	CAAAAAATTATACCTTTAATGTCCTAAACCAATTCAGTACTTGTTCATCTCTTCAAAGTGATAT	1370	
QY	842	CTTTCCTGGTTTCAGCTTATTTAATGATAAAAA	873	
Db	1371	CTCACTCTTTTCTGTTTCGTTTATGCTCATAAA	1402	

```

RESULT 4
US-09-925-065A-553911
, Sequence 553911, Application US/09925065A
, Publication No. US20040181048A1
, GENERAL INFORMATION:
,
, APPLICANT: Wang, David G.
,
, TITLE OF INVENTION: Identification and Mapping of Single
,
, TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
,
, FILE REFERENCE: 108827.135
,
, CURRENT APPLICATION NUMBER: US/09/925,065A
,
, CURRENT FILING DATE: 2001-08-08
,
, PRIOR APPLICATION NUMBER: US 60/243,096
,
, PRIOR FILING DATE: 2000-10-24
,
, PRIOR APPLICATION NUMBER: US 60/252,147
,
, PRIOR FILING DATE: 2000-11-20
,
, PRIOR APPLICATION NUMBER: US 60/250,092
,
, PRIOR FILING DATE: 2000-11-30
,
, PRIOR APPLICATION NUMBER: US 60/261,766
,
, PRIOR FILING DATE: 2001-01-16
,
, PRIOR APPLICATION NUMBER: US 60/289,846
,
, PRIOR FILING DATE: 2001-05-09
,
, NUMBER OF SEQ IDS NOS: 957086
,
, SOFTWARE: FASTSEQ for Windows Version 4.0

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PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 265276  
LENGTH: 483  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-285276

Query Match  
Best Local Similarity 48.2%; Pred. No. 8.8; DB 6; Length 483;  
Matches 109; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 639 AGCAGTCATGAGATGGAGACCTTCATTCCTCCCAAGCAGAAACGAAATGGAGAGA 698  
DB 208 AGAAGCTACTATAGCATATCTATTTACACAACTAGAGGAATGAATTAATGGA 267  
QY 699 ACAATTGAGCCAGAGTTTGAAGAAATAAGATGGTTGATGAAGAGTGGACATAGATT 758  
DB 268 ACAAGAGGAATTGAACAAGGAGACTGAAACAAAGTTGAACAAGGAGGAAACAGAAATATT 327  
QY 759 GAAAAATACAGAAATAGTTTGAACAAATAACATTTATGCAAGCCCTTACAACTATTGCT 818  
DB 328 GAATAGACAGAGCAAGCAAGTAAATGAAGCAGTAATTAACAACTACCAGTCAATA 387  
QY 819 TGAAGTAGAACAGAGATAAGAACTTTCTCGTTTCAGCTTATTAA 864  
DB 388 AGCCTGAAATGAGAAAGAGGACTCTCTTAACTATCTATATA 433

RESULT 11  
US-09-925-065A-597659  
; Sequence 597659, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 597659  
; LENGTH: 528  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-597659

Query Match  
Best Local Similarity 49.0%; Pred. No. 9.1;  
Matches 103; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 36 AACACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTTGGCATGTCTCCGCAACGATTGCA 95

DB 255 ACCACTGAGTCAACCTATATTTCCAAACAAATCTCGGGAATAGCTCGCAATACACA 314  
QY 96 GACCAAGAACTGGGTGATGCCCAATTCCTTGACCGGCTTCGCCGAGACGAGATCCCTTA 155  
DB 315 GACTAAAAAGATGGCGCTCCCAACCCCAAAACACCTTCCCTACCCACAGCCTCTGCTC 374  
QY 156 AAAGGAAGAGGTAGCACTCTTGTCTGGAATCGAATCGAAGCAGCACTCGTGGAGGAAGG 215  
DB 375 AAAATACCCACCAACAACTTGAATTTTAAATCTAAGGAAGAAATCAAGCAGATGACTA 434  
QY 216 ATAGTGAGCAGATTCCTGGAAGAGGAATCA 245  
DB 435 TGATTGAAGCTTATTTTGTATAGCAATGA 464

RESULT 12  
US-09-925-065A-279044/c  
; Sequence 279044, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 279044  
; LENGTH: 549  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-279044

Query Match  
Best Local Similarity 4.3%; Score 38.4; DB 6; Length 549;  
Matches 96; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 576 GCACCTTAATGGAATGATTAATACGGTTAGAACTCTCGAAACTCTACAGATTCGCTTGG 635  
DB 193 GGATTAACCTTGGATTATGATAGTGGTTTATATCTTAATATCTCCAGTGGTTGTTGA 134  
QY 636 AGAAGCAGTCATGAGATGGGAGACCTTCATTCCTCCAAAGCAGAAACGAAATCGAG 695  
DB 133 AGAATTAAGTCATATTTTAGAAAAATTTGTAATGGAATAAATTAACACTTATTATATTC 74  
QY 696 AGAACAAATGAGCCAGAGTTTGAAGAAATAAGATGGTTGATTTGAAGAGTGGCAGATAG 755  
DB 73 AGCAGTATATCTATATTTCTTCCAAAGAAATCTGAGTGTCTTGAGAGTTGTGTCTATTG 14  
QY 756 ATTGAAAAATAC 767  
DB 13 ACCAGAAATTC 2

RESULT 13  
US-09-925-065A-279045/c  
; Sequence 279045, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single



;; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
;; FILE REFERENCE: 108827.135  
;; CURRENT APPLICATION NUMBER: US/09/925,065A  
;; CURRENT FILING DATE: 2001-08-08  
;; PRIOR APPLICATION NUMBER: US 60/243,096  
;; PRIOR FILING DATE: 2000-10-24  
;; PRIOR APPLICATION NUMBER: US 60/252,147  
;; PRIOR FILING DATE: 2000-11-20  
;; PRIOR APPLICATION NUMBER: US 60/250,092  
;; PRIOR FILING DATE: 2000-11-30  
;; PRIOR APPLICATION NUMBER: US 60/261,766  
;; PRIOR FILING DATE: 2001-01-16  
;; PRIOR APPLICATION NUMBER: US 60/289,846  
;; PRIOR FILING DATE: 2001-05-09  
;; NUMBER OF SEQ ID NOS: 957086  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
;; SEQ ID NO 279045  
;; LENGTH: 549  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; US-09-925-065A-279045

Query Match 4.3%; Score 38.4; DB 6; Length 549;  
Best Local Similarity 50.0%; Pred. No. 12;  
Matches 96; Conservative 0; Mismatches 96; Indels 0; Gaps 0;  
QY 576 GGACTTAATGAAGTAAATACGGTTAGAACTCTCGAACTCTACAGAGATTCGCTTGG 635  
DB 193 GGATTAACCTTGGATATGATAGTGGTTTATTATCTAATTAATCTCCAGTGGTTGTTGA 134  
QY 636 AGAAGCAGTCATGAGAAATGCGAGACCTTCATCCCTCCAAAGCAGAAACGAAAAATGGAG 695  
DB 133 AGAATTAAGAGTCATATTAGAAAAATTTGGAATGGAATAAACAACCTATTATATTC 74  
QY 696 AGAACAAATGAGCAGAGTTTGAAGAAATAAGATGTTGATGAAGAGTGCACATAG 755  
DB 73 AGGCAGTACTATATTTCTCCAAAGAGATCTGAGTCTTTGAGAGTTGTGTCATTG 14  
QY 756 ATTGAATAATAC 767  
DB 13 AACCAAGAAATTC 2

RESULT 14  
US-09-925-065A-766520  
; Sequence 766520, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 766520  
; LENGTH: 623  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-925-065A-766520

Query Match 4.3%; Score 38.4; DB 6; Length 623;

Best Local Similarity 53.3%; Pred. No. 12;  
Matches 81; Conservative 0; Mismatches 71; Indels 0; Gaps 0;  
QY 644 TCATGAGATGGAGACCTTCATTCCTCCAAAGCAGAAACGAAAAATCGAGAGAACAT 703  
DB 174 TTATGAAATTCBAACCTTTTGTCTGTGAAGACAGCATTTGAAAGCAAGCAAG 233  
QY 704 TGAGCCAGAGATTTGAAGAAATAAGATGTTGATTTGAAGAGTGCACATAGATTGAAA 763  
DB 234 CCAGACACTTGGTTAAAGTATATGTTGATAAAGATGTATCCAGTATATATAATAA 293  
QY 764 ATACAGAAAATAGTTTTGAACAAATAACATTT 795  
DB 294 CTCCTTAACCTCAGCAATAAACAACAACACTTT 325

RESULT 15  
US-09-925-065A-771317  
; Sequence 771317, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 771317  
; LENGTH: 631  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-925-065A-771317

Query Match 4.3%; Score 38.4; DB 6; Length 631;  
Best Local Similarity 53.3%; Pred. No. 12;  
Matches 81; Conservative 0; Mismatches 71; Indels 0; Gaps 0;  
QY 644 TCATGAGATGGAGACCTTCATTCCTCCAAAGCAGAAACGAAAAATCGAGAGAACAT 703  
DB 182 TTATGAAATTCBAACCTTTTGTCTGTGAAGACAGCATTTGAAAGCAAGCAAG 241  
QY 704 TGAGCCAGAGATTTGAAGAAATAAGATGTTGATTTGAAGAGTGCACATAGATTGAAA 763  
DB 242 CCAGACACTTGGTTAAAGTATATGTTGATAAAGATGTATCCAGTATATATAATAA 301  
QY 764 ATACAGAAAATAGTTTTGAACAAATAACATTT 795  
DB 302 CTCCTTAACCTCAGCAATAAACAACAACACTTT 333

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Job time : 418.426 secs

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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 00:58:01 ; Search time 715.798 Seconds  
(without alignments)  
7971.337 Million cell updates/sec

Title: US-10-734-373-59  
Perfect score: 690  
Sequence: 1 atgattccaacactgtgc.....gaacaattgaccagaagt 690

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries





Db 61 CGATTTCAGACCAAGAACTGGGTGATGCCCCCACTTCCTTGACCGCTTCGCCGAGACGAG 120  
Qy 121 AAGTCCCTAAAAGAGAGAGTGTAGTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180  
Db 121 AAGTCCCTAAAAGAGAGAGTGTAGTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180  
Qy 181 GGAAGAGAGTGTAGTGTAGTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 240  
Db 181 GGAAGAGAGTGTAGTGTAGTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 240  
Qy 241 ATTGCCTCTGTCTGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGT 300  
Db 241 ATTGCCTCTGTCTGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGT 300  
Qy 301 GACTGTTTCACTGCTCATGCCCCAAGCAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 360  
Db 301 GACTGTTTCACTGCTCATGCCCCAAGCAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 360  
Qy 361 CAGGCAATCATGATTAAGAAATCACTTAAAGCAAACTTTAGTGTGATTTTGAAGG 420  
Db 361 CAGGCAATCATGATTAAGAAATCACTTAAAGCAAACTTTAGTGTGATTTTGAAGG 420  
Qy 421 CTGGAGACACTAATACTTCTTCAAGGCTTTCACCGAAGAGAGAGTGTGCGGAAAT 480  
Db 421 CTGGAGACACTAATACTTCTTCAAGGCTTTCACCGAAGAGAGAGTGTGCGGAAAT 480  
Qy 481 TCACCATTCCTTCTTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGTC 540  
Db 481 TCACCATTCCTTCTTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGTC 540  
Qy 541 CTATCGGAGAGTCTTAAATGGAATGATTAAGTGTGATTTTGAAGTCTTCAAGG 600  
Db 541 CTATCGGAGAGTCTTAAATGGAATGATTAAGTGTGATTTTGAAGTCTTCAAGG 600  
Qy 601 TTGCTTGGAGAGAGTCTTAAATGGAATGATTAAGTGTGATTTTGAAGTCTTCAAGG 660  
Db 601 TTGCTTGGAGAGAGTCTTAAATGGAATGATTAAGTGTGATTTTGAAGTCTTCAAGG 660  
Qy 661 AAAATGGAGAGAACTTGAAGGAGT 690  
Db 661 AAAATGGAGAGAACTTGAAGGAGT 690

RESULT 6  
US-10-181-585B-41  
; Sequence 41, Application US/10181585B  
; Publication No. US20050175985A1  
; GENERAL INFORMATION:  
; APPLICANT: The University of Pittsburgh - of the Commonwealth System  
; APPLICANT: Of Higher Education  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C3-PUS  
; CURRENT APPLICATION NUMBER: US/10/181,585B  
; PRIOR FILING DATE: 2003-12-08  
; PRIOR APPLICATION NUMBER: PCT/US01/05048  
; PRIOR FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: 09/506,286  
; PRIOR FILING DATE: 2000-02-16  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 41  
; LENGTH: 690  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-10-181-585B-41

Query Match 100.0%; Score 690; DB 9; Length 690;  
Best Local Similarity 100.0%; Pred. No. 1.4e-206;  
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGATTCCAAACACATGTGTCAAGCTTTCAAGGTAGACTGTTTCTTTGGCATGTCCGAAA 60  
Db 1 ATGGATTCCAAACACATGTGTCAAGCTTTCAAGGTAGACTGTTTCTTTGGCATGTCCGAAA 60  
Qy 61 CGATTTTGCAGACCAAGAACTGGGTGATGCCCCCACTTCCTTGACCGCTTCGCCGAGACGAG 120  
Db 61 CGATTTTGCAGACCAAGAACTGGGTGATGCCCCCACTTCCTTGACCGCTTCGCCGAGACGAG 120  
Qy 121 AAGTCCCTAAAAGAGAGAGTGTAGTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180  
Db 121 AAGTCCCTAAAAGAGAGAGTGTAGTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180  
Qy 181 GGAAGAGAGTGTAGTGTAGTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 240  
Db 181 GGAAGAGAGTGTAGTGTAGTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 240  
Qy 241 ATTGCCTCTGTCTGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGT 300  
Db 241 ATTGCCTCTGTCTGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGT 300  
Qy 301 GACTGTTTCACTGCTCATGCCCCAAGCAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 360  
Db 301 GACTGTTTCACTGCTCATGCCCCAAGCAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 360  
Qy 361 CAGGCAATCATGATTAAGAAATCACTTAAAGCAAACTTTAGTGTGATTTTGAAGG 420  
Db 361 CAGGCAATCATGATTAAGAAATCACTTAAAGCAAACTTTAGTGTGATTTTGAAGG 420  
Qy 421 CTGGAGACACTAATACTTCTTCAAGGCTTTCACCGAAGAGAGAGTGTGCGGAAAT 480  
Db 421 CTGGAGACACTAATACTTCTTCAAGGCTTTCACCGAAGAGAGAGTGTGCGGAAAT 480  
Qy 481 TCACCATTCCTTCTTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGTC 540  
Db 481 TCACCATTCCTTCTTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGTC 540  
Qy 541 CTATCGGAGAGTCTTAAATGGAATGATTAAGTGTGATTTTGAAGTCTTCAAGG 600  
Db 541 CTATCGGAGAGTCTTAAATGGAATGATTAAGTGTGATTTTGAAGTCTTCAAGG 600  
Qy 601 TTGCTTGGAGAGAGTCTTAAATGGAATGATTAAGTGTGATTTTGAAGTCTTCAAGG 660  
Db 601 TTGCTTGGAGAGAGTCTTAAATGGAATGATTAAGTGTGATTTTGAAGTCTTCAAGG 660  
Qy 661 AAAATGGAGAGAACTTGAAGGAGT 690  
Db 661 AAAATGGAGAGAACTTGAAGGAGT 690

RESULT 7  
US-10-065-133A-53  
; Sequence 53, Application US/10065133A  
; Publication No. US20030199074A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; PRIOR FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 53  
; LENGTH: 888  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-10-065-133A-53

Query Match 100.0%; Score 690; DB 6; Length 888;



;; PRIOR FILING DATE: 1998-08-13  
;; NUMBER OF SEQ ID NOS: 108  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 53  
;; LENGTH: 888  
;; TYPE: DNA  
;; ORGANISM: Equine influenza virus H3N8  
US-10-734-373-59

Query Match 100.0%; Score 690; DB 7; Length 888;  
Best Local Similarity 100.0%; Pred. No. 1.6e-206; Indels 0; Gaps 0;  
Matches 690; Conservative 0; Mismatches 0;

QY 1 ATGGATTCACACATGCTCAAGCTTTCAGGTAGACTGTTTCTTGGCATGTCCGCAA 60  
DB 25 ATGGATTCACACATGCTCAAGCTTTCAGGTAGACTGTTTCTTGGCATGTCCGCAA 84  
QY 61 CGATTTGCGAGCAAGAACTGGGTGATGCCCATTCCTTGCAGCGCTTCGCGAGACG 120  
DB 85 CGATTTGCGAGCAAGAACTGGGTGATGCCCATTCCTTGCAGCGCTTCGCGAGACG 144  
QY 121 AAGTCCCTAAAAGGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGA 180  
DB 145 AAGTCCCTAAAAGGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGA 204  
QY 181 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACC 240  
DB 205 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACC 264  
QY 241 ATTGCCTCTGTTCTCTGCTTACCGCTACTTAACCTGACATGACTCTTGTGAGATGTCAGA 300  
DB 265 ATTGCCTCTGTTCTCTGCTTACCGCTACTTAACCTGACATGACTCTTGTGAGATGTCAGA 324  
QY 301 GACTGGTTCATGCTCATGCCCCAGCAAGAAAGTAAACAGGCTCCCTTAATGATATAAGAAATGGAC 360  
DB 325 GACTGGTTCATGCTCATGCCCCAGCAAGAAAGTAAACAGGCTCCCTTAATGATATAAGAAATGGAC 384  
QY 361 CAGCAATCATGATAAGAAACATCATACTTAAAGCAAACTTTAGTGTGATTTTTCGAAAGG 420  
DB 385 CAGCAATCATGATAAGAAACATCATACTTAAAGCAAACTTTAGTGTGATTTTTCGAAAGG 444  
QY 421 CTGGAGACACTAATACTACTTAGAGCCTTACCGAAGAGGAGCAGTCTGTTGGCGAAATT 480  
DB 445 CTGGAGACACTAATACTACTTAGAGCCTTACCGAAGAGGAGCAGTCTGTTGGCGAAATT 504  
QY 481 TCACCATTCCTCTCTCCAGGACATCTAATGAGGATGTCAAAAATGCAATTGGGGTC 540  
DB 505 TCACCATTCCTCTCTCCAGGACATCTAATGAGGATGTCAAAAATGCAATTGGGGTC 564  
QY 541 CTGATCGGAGCTTAAATGGAATGATAACGGTTTNGAATCTCTGAACTCTACAGAGA 600  
DB 565 CTGATCGGAGCTTAAATGGAATGATAACGGTTTNGAATCTCTGAACTCTACAGAGA 624  
QY 601 TTCCTTTGGAGAGCAGTCAATGAGAGCTTCAATTCCTCCCAAGCAGAAACGA 660  
DB 625 TTCCTTTGGAGAGCAGTCAATGAGAGCTTCAATTCCTCCCAAGCAGAAACGA 684  
QY 661 AAAATGGAGAGCAAAATGAGCCAGAGTT 690  
DB 685 AAAATGGAGAGCAAAATGAGCCAGAGTT 714

RESULT 10  
US-10-734-373-57  
; Sequence 57, Application US/10734373  
; Publication No. US20040137015A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/734,373  
; CURRENT FILING DATE: 2003-12-12

;; PRIOR APPLICATION NUMBER: PCT/US99/18583  
;; PRIOR FILING DATE: 1999-08-12  
;; PRIOR APPLICATION NUMBER: 09/133,921  
;; PRIOR FILING DATE: 1998-08-13  
;; NUMBER OF SEQ ID NOS: 108  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 57  
;; LENGTH: 888  
;; TYPE: DNA  
;; ORGANISM: Equine influenza virus H3N8  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (27)..(716)  
;; OTHER INFORMATION:  
US-10-734-373-57

Query Match 100.0%; Score 690; DB 7; Length 888;  
Best Local Similarity 100.0%; Pred. No. 1.6e-206; Indels 0; Gaps 0;  
Matches 690; Conservative 0; Mismatches 0;

QY 1 ATGGATTCACACATGCTCAAGCTTTCAGGTAGACTGTTTCTTGGCATGTCCGCAA 60  
DB 27 ATGGATTCACACATGCTCAAGCTTTCAGGTAGACTGTTTCTTGGCATGTCCGCAA 86  
QY 61 CGATTTGCGAGCAAGAACTGGGTGATGCCCATTCCTTGCAGCGCTTCGCGAGACG 120  
DB 87 CGATTTGCGAGCAAGAACTGGGTGATGCCCATTCCTTGCAGCGCTTCGCGAGACG 146  
QY 121 AAGTCCCTAAAAGGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGA 180  
DB 147 AAGTCCCTAAAAGGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGA 206  
QY 181 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACC 240  
DB 207 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACC 266  
QY 241 ATTGCCTCTGTTCTCTGCTTACCGCTACTTAACCTGACATGACTCTTGTGAGATGTCAGA 300  
DB 267 ATTGCCTCTGTTCTCTGCTTACCGCTACTTAACCTGACATGACTCTTGTGAGATGTCAGA 326  
QY 301 GACTGGTTCATGCTCATGCCCCAGCAAGAAAGTAAACAGGCTCCCTTAATGATATAAGAAATGGAC 360  
DB 327 GACTGGTTCATGCTCATGCCCCAGCAAGAAAGTAAACAGGCTCCCTTAATGATATAAGAAATGGAC 386  
QY 361 CAGCAATCATGATAAGAAACATCATACTTAAAGCAAACTTTAGTGTGATTTTTCGAAAGG 420  
DB 387 CAGCAATCATGATAAGAAACATCATACTTAAAGCAAACTTTAGTGTGATTTTTCGAAAGG 446  
QY 421 CTGGAGACACTAATACTACTTAGAGCCTTACCGAAGAGGAGCAGTCTGTTGGCGAAATT 480  
DB 447 CTGGAGACACTAATACTACTTAGAGCCTTACCGAAGAGGAGCAGTCTGTTGGCGAAATT 506  
QY 481 TCACCATTCCTCTCTCCAGGACATCTAATGAGGATGTCAAAAATGCAATTGGGGTC 540  
DB 507 TCACCATTCCTCTCTCCAGGACATCTAATGAGGATGTCAAAAATGCAATTGGGGTC 566  
QY 541 CTCATCGGAGCTTAAATGGAATGATAACGGTTTNGAATCTCTGAACTCTACAGAGA 600  
DB 567 CTCATCGGAGCTTAAATGGAATGATAACGGTTTNGAATCTCTGAACTCTACAGAGA 626  
QY 601 TTCCTTTGGAGAGCAGTCAATGAGAGCTTCAATTCCTCCCAAGCAGAAACGA 660  
DB 627 TTCCTTTGGAGAGCAGTCAATGAGAGCTTCAATTCCTCCCAAGCAGAAACGA 686  
QY 661 AAAATGGAGAGCAAAATGAGCCAGAGTT 690  
DB 687 AAAATGGAGAGCAAAATGAGCCAGAGTT 716

RESULT 11  
US-10-181-585B-35  
; Sequence 35, Application US/10181585B  
; Publication No. US20050175965A1



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; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System
; APPLICANT: Of Higher Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C3-PUS
; CURRENT APPLICATION NUMBER: US/10/181.585B
; PRIOR FILING DATE: 2003-12-08
; PRIOR FILING DATE: 2001-02-16
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 35
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-181-585B-35

Query Match      100.0%; Score 690; DB 9; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.6e-206;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGATTCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCCAAA 60
Db 25 ATGGATTCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCCAAA 84

Qy 61 CGATTTCGAGACCAAGAACTGGGTGATGCCCTTCTTGCACGGCTTCGCCGAGACCAAG 120
Db 85 CGATTTCGAGACCAAGAACTGGGTGATGCCCTTCTTGCACGGCTTCGCCGAGACCAAG 144

Qy 121 AAGTCCCTTAAAGGAAGAGGTAGACTCTTGGTCTGACATCGAAACAGGCACCTCGTGCA 180
Db 145 AAGTCCCTTAAAGGAAGAGGTAGACTCTTGGTCTGACATCGAAACAGGCACCTCGTGCA 204

Qy 181 GGAAGCAGATAGTGGAGCAGATCTCGGAGAGGAAATCAGATGAGGCACCTTAAATGACC 240
Db 205 GGAAGCAGATAGTGGAGCAGATCTCGGAGAGGAAATCAGATGAGGCACCTTAAATGACC 264

Qy 241 ATTGCCTCTGTTCTGCTTCAAGCAGAAATCTTAAAGCAAACTTTAGTGTGATTTGCAAGG 300
Db 265 ATTGCCTCTGTTCTGCTTCAAGCAGAAATCTTAAAGCAAACTTTAGTGTGATTTGCAAGG 324

Qy 301 GACTGGTTCATGCTGATGCCGAGCAGAAATCTTAAAGCAAACTTTAGTGTGATTTGCAAGG 360
Db 325 GACTGGTTCATGCTGATGCCGAGCAGAAATCTTAAAGCAAACTTTAGTGTGATTTGCAAGG 384

Qy 361 CAGGCAATCATGATTAAGAAATCATATCTTAAAGCAAACTTTAGTGTGATTTGCAAGG 420
Db 385 CAGGCAATCATGATTAAGAAATCATATCTTAAAGCAAACTTTAGTGTGATTTGCAAGG 444

Qy 421 CTGGAGACATTAATATCTTATAGCCCTTCAACGAGAAAGGAGCAGTCTTGGCGCAAAAT 480
Db 445 CTGGAGACATTAATATCTTATAGCCCTTCAACGAGAAAGGAGCAGTCTTGGCGCAAAAT 504

Qy 481 TCACCATTTGCTTCTCTTCCAGGACATATAATGAGGATGTCAAAATATGCAATTTGGGGTC 540
Db 505 TCACCATTTGCTTCTCTTCCAGGACATATAATGAGGATGTCAAAATATGCAATTTGGGGTC 564

Qy 541 CTCATCGGAGACTTAAATGGAATGATAATACGGTTAGAACTCTTGAACCTCTACAGAGA 600
Db 565 CTCATCGGAGACTTAAATGGAATGATAATACGGTTAGAACTCTTGAACCTCTACAGAGA 624

Qy 601 TTCCGCTTGGAGAGCAGTCTAGAAATGGGAGACCTTCAATCCCTCCAAAGCAGAAACGA 660
Db 625 TTCCGCTTGGAGAGCAGTCTAGAAATGGGAGACCTTCAATCCCTCCAAAGCAGAAACGA 684

Qy 661 AAATGGAGAGCAANTTGAACCAAGTT 690
Db 685 AAATGGAGAGCAANTTGAACCAAGTT 714
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RESULT 12
US-10-181-585B-39
; Sequence 39, Application US/10181585B
; Publication No. US20050175985A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System
; APPLICANT: Of Higher Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C3-PUS
; CURRENT APPLICATION NUMBER: US/10/181.585B
; CURRENT FILING DATE: 2003-12-08
; PRIOR FILING DATE: 2001-02-16
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 39
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(716)
US-10-181-585B-39
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Query Match      100.0%; Score 690; DB 9; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.6e-206;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGATTCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCCAAA 60
Db 27 ATGGATTCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCCAAA 86

Qy 61 CGATTTCGAGACCAAGAACTGGGTGATGCCCTTCTTGCACGGCTTCGCCGAGACCAAG 120
Db 87 CGATTTCGAGACCAAGAACTGGGTGATGCCCTTCTTGCACGGCTTCGCCGAGACCAAG 146

Qy 121 AAGTCCCTTAAAGGAAGAGGTAGACTCTTGGTCTGACATCGAAACAGGCACCTCGTGCA 180
Db 147 AAGTCCCTTAAAGGAAGAGGTAGACTCTTGGTCTGACATCGAAACAGGCACCTCGTGCA 206

Qy 181 GGAAGCAGATAGTGGAGCAGATCTCGGAGAGGAAATCAGATGAGGCACCTTAAATGACC 240
Db 207 GGAAGCAGATAGTGGAGCAGATCTCGGAGAGGAAATCAGATGAGGCACCTTAAATGACC 266

Qy 241 ATTGCCTCTGTTCTGCTTCAAGCAGAAATCTTAAAGCAAACTTTAGTGTGATTTGCAAGA 300
Db 267 ATTGCCTCTGTTCTGCTTCAAGCAGAAATCTTAAAGCAAACTTTAGTGTGATTTGCAAGA 326

Qy 301 GACTGGTTCATGCTGATGCCCAAGCAGAAAGTAAAGCAAACTTTAGTGTGATTTGCAAGG 360
Db 327 GACTGGTTCATGCTGATGCCCAAGCAGAAAGTAAAGCAAACTTTAGTGTGATTTGCAAGG 386

Qy 361 CAGGCAATCATGATTAAGAAATCATATCTTAAAGCAAACTTTAGTGTGATTTGCAAGG 420
Db 387 CAGGCAATCATGATTAAGAAATCATATCTTAAAGCAAACTTTAGTGTGATTTGCAAGG 446

Qy 421 CTGGAGACATTAATATCTTATAGCCCTTCAACGAGAAAGGAGCAGTCTTGGCGCAAAAT 480
Db 447 CTGGAGACATTAATATCTTATAGCCCTTCAACGAGAAAGGAGCAGTCTTGGCGCAAAAT 506

Qy 481 TCACCATTTGCTTCTCTTCCAGGACATATAATGAGGATGTCAAAATATGCAATTTGGGGTC 540
Db 507 TCACCATTTGCTTCTCTTCCAGGACATATAATGAGGATGTCAAAATATGCAATTTGGGGTC 566

Qy 541 CTCATCGGAGACTTAAATGGAATGATAATACGGTTAGAACTCTTGAACCTCTACAGAGA 600
Db 567 CTCATCGGAGACTTAAATGGAATGATAATACGGTTAGAACTCTTGAACCTCTACAGAGA 626
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QY 601 TTGCTTTGGAGAGCAGTCATGAGATGGAGAGCCTTCATTCCCTCCAAAGCAGAAACGA 660  
Db 627 TTGCTTTGGAGAGCAGTCATGAGATGGAGAGCCTTCATTCCCTCCAAAGCAGAAACGA 686  
QY 661 AAAATGGAGAGAACTTTGAGCCAGAGATT 690  
Db 687 AAAATGGAGAGAACTTTGAGCCAGAGATT 716  
RESULT 13  
US-10-065-133A-50  
; Sequence 50, Application US/10065133A  
; Publication No. US20030199074A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; PRIOR FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 50  
; LENGTH: 891  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (27)..(716)  
; OTHER INFORMATION:  
US-10-065-133A-50  
Query Match 100.0%; Score 690; DB 6; Length 891;  
Best Local Similarity 100.0%; Pred. No. 1.6e-206;  
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGATTCCAAACACTGTGTCAAGCTTTTCAGGTAGACTGTTTTCTTTGGCATGTCCGCAAA 60  
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QY 61 CGATTTGCAGACCAAGAACTGGGTGATGCCCATTCCTTTGACCGGCTTCGCCGAGACCAG 120  
Db 87 CGATTTGCAGACCAAGAACTGGGTGATGCCCATTCCTTTGACCGGCTTCGCCGAGACCAG 146  
QY 121 AAGTCCCTTAAAGGAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180  
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QY 181 GGAAGCAGATAGTGGAGCAGATTCGAGAGAGATCAGATGAGGCACCTTAAATGACC 240  
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QY 241 ATTGCCTCTGCTTCAGCTTACCTTAACTGATGAGTCTTGTGATGAGATGTCAGA 300  
Db 267 ATTGCCTCTGCTTCAGCTTACCTTAACTGATGAGTCTTGTGATGAGATGTCAGA 326  
QY 301 GACTGGTTCATGCTATGCCCAAGCAGAACTTAAAGCAAACTTTAGTGTGATTTTCAAGG 420  
Db 327 GACTGGTTCATGCTATGCCCAAGCAGAACTTAAAGCAAACTTTAGTGTGATTTTCAAGG 446  
QY 361 CAGGCAATCATGATTAAGAACTTAAAGCAAACTTTAGTGTGATTTTCAAGG 480  
Db 387 CAGGCAATCATGATTAAGAACTTAAAGCAAACTTTAGTGTGATTTTCAAGG 506  
QY 421 CTTGAGAGCACTAATCTTCTAGAGCCTTCAACCGAAGAGAGAGCAGTCTGTTGGCGAAATT 480  
Db 447 CTTGAGAGCACTAATCTTCTAGAGCCTTCAACCGAAGAGAGAGCAGTCTGTTGGCGAAATT 506  
QY 481 TCACCATTCGCTTCTCTCTCCAGGACATACATAATGAGGATGTCAAAAATGCAATTTGGGGTC 540

Db 507 TCACCATTCGCTTCTCTCTCCAGGACATACATAATGAGGATGTCAAAAATGCAATTTGGGGTC 566  
QY 541 CTATCGGAGAGCTTAAATGGAATGATATACGGTTAGAACTCTGTAAGTCTTACAGAGA 600  
Db 567 CTATCGGAGAGCTTAAATGGAATGATATACGGTTAGAACTCTGTAAGTCTTACAGAGA 626  
QY 601 TTGCTTTGGAGAGCAGTCATGAGATGGAGAGCCTTCATTCCCTCCAAAGCAGAAACGA 660  
Db 627 TTGCTTTGGAGAGCAGTCATGAGATGGAGAGCCTTCATTCCCTCCAAAGCAGAAACGA 686  
QY 661 AAAATGGAGAGAACTTTGAGCCAGAGATT 690  
Db 687 AAAATGGAGAGAACTTTGAGCCAGAGATT 716  
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; Sequence 50, Application US/10734373  
; Publication No. US20040137015A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/734,373  
; PRIOR FILING DATE: 2003-12-12  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 50  
; LENGTH: 891  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (27)..(716)  
; OTHER INFORMATION:  
US-10-734-373-50  
Query Match 100.0%; Score 690; DB 7; Length 891;  
Best Local Similarity 100.0%; Pred. No. 1.6e-206;  
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGATTCCAAACACTGTGTCAAGCTTTTCAGGTAGACTGTTTTCTTTGGCATGTCCGCAAA 60  
Db 27 ATGGATTCCAAACACTGTGTCAAGCTTTTCAGGTAGACTGTTTTCTTTGGCATGTCCGCAAA 86  
QY 61 CGATTTGCAGACCAAGAACTGGGTGATGCCCATTCCTTTGACCGGCTTCGCCGAGACCAG 120  
Db 87 CGATTTGCAGACCAAGAACTGGGTGATGCCCATTCCTTTGACCGGCTTCGCCGAGACCAG 146  
QY 121 AAGTCCCTTAAAGGAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180  
Db 147 AAGTCCCTTAAAGGAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 206  
QY 181 GGAAGCAGATAGTGGAGCAGATTCGAGAGAGATCAGATGAGGCACCTTAAATGACC 240  
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QY 241 ATTGCCTCTGCTTCAGCTTACCTTAACTGATGAGTCTTGTGATGAGATGTCAGA 300  
Db 267 ATTGCCTCTGCTTCAGCTTACCTTAACTGATGAGTCTTGTGATGAGATGTCAGA 326  
QY 301 GACTGGTTCATGCTATGCCCAAGCAGAACTTAAAGCAAACTTTAGTGTGATTTTCAAGG 360  
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QY 361 CAGGCAATCATGATTAAGAACTTAAAGCAAACTTTAGTGTGATTTTCAAGG 420



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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 22:34:28 ; Search time 230.875 Seconds  
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5312.485 Million cell updates/sec

Title: US-10-734-373-59

Perfect score: 690

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Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888760828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	690	100.0	690	3	US-10-065-133A-59
5	690	100.0	888	3	US-09-506-286B-53
6	690	100.0	888	3	US-09-506-286B-57
7	690	100.0	888	3	US-10-065-133A-53
8	690	100.0	888	3	US-10-065-133A-57
9	690	100.0	891	3	US-09-506-286B-50
10	690	100.0	891	3	US-10-065-133A-50
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12	291.4	42.2	293	3	US-09-506-286B-56
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14	291.4	42.2	468	3	US-09-506-286B-54
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17	212.8	30.8	918	6	PCT-US94-01149-58
18	212	30.7	453	2	US-08-388-267C-3
19	212	30.7	453	3	US-09-277-720-3
20	212	30.7	690	6	PCT-US94-01149-11
21	212	30.7	690	6	PCT-US94-01149-71
22	212	30.7	924	6	PCT-US94-01149-15
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24	211.6	30.7	717	6	PCT-US94-01149-23

25	211.6	30.7	729	6	PCT-US94-01149-17	Sequence 17, Appl
26	211.6	30.7	912	6	PCT-US94-01149-31	Sequence 31, Appl
27	210.4	30.5	1014	2	US-08-441-857-7	Sequence 7, Appl
28	210.4	30.5	1014	3	US-08-193-159-7	Sequence 7, Appl
29	210.4	30.5	1014	3	US-09-283-646C-7	Sequence 7, Appl
30	210.4	30.5	1017	2	US-08-441-857-9	Sequence 9, Appl
31	210.4	30.5	1017	2	US-08-441-857-11	Sequence 11, Appl
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33	210.4	30.5	1017	3	US-08-193-159-11	Sequence 11, Appl
34	210.4	30.5	1017	3	US-09-283-646C-9	Sequence 9, Appl
35	210.4	30.5	1017	3	US-09-283-646C-11	Sequence 11, Appl
36	210.4	30.5	1020	2	US-08-441-857-5	Sequence 5, Appl
37	210.4	30.5	1020	2	US-08-193-159-5	Sequence 5, Appl
38	210.4	30.5	1020	3	US-09-283-646C-5	Sequence 5, Appl
39	208.8	30.3	915	6	PCT-US94-01149-56	Sequence 56, Appl
40	208.8	30.3	915	6	PCT-US94-01149-54	Sequence 54, Appl
41	112.6	16.2	630	6	PCT-US94-01149-13	Sequence 13, Appl
42	112.6	16.2	630	6	PCT-US94-01149-21	Sequence 21, Appl
43	112	16.2	810	2	PCT-US94-01149-19	Sequence 19, Appl
44	39.4	5.7	7218	2	US-08-232-463-14	Sequence 14, Appl
45	39.2	5.7	601	3	US-09-949-016-152799	Sequence 152799,

## ALIGNMENTS

## RESULT 1

US-09-506-286B-52

; Sequence 52, Application US/09506286B

; Patent No. 6482414

; GENERAL INFORMATION:

; APPLICANT: Dowling, Patricia W.

; APPLICANT: Youngner, Julius S.

; APPLICANT: The University of Pittsburgh, of the Commonwealth

; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES

; FILE REFERENCE: EQ-1-C2

; CURRENT APPLICATION NUMBER: US/09/506,286B

; PRIOR FILING DATE: 2000-02-16

; PRIOR FILING DATE: 1998-08-13

; PRIOR FILING DATE: 1999-08-12

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 52

; LENGTH: 690

; TYPE: DNA

; ORGANISM: Equine influenza virus H3N8

US-09-506-286B-52

Query Match	100.0%	Score 690;	DB 3;	Length 690;
Best Local Similarity	100.0%;	Pred. No. 1.6e-212;	Mismatches 0;	Indels 0;
Matches 690;	Conservative 0;			Gaps 0;
QY	1	ATGGATTCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA	60	
DB	1	ATGGATTCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA	60	
QY	61	CGATTTCAGACCAAGAACTGGGTGATGCCCCCATTCCTTGACCCGGTTCGCCGAGACGAG	120	
DB	61	CGATTTCAGACCAAGAACTGGGTGATGCCCCCATTCCTTGACCCGGTTCGCCGAGACGAG	120	
QY	121	AAAGTCCCTTAAAGGAAGAGGAGTAGCACTCTTGTCTGGACATCGAAACAGCCACTCGTGCA	180	
DB	121	AAAGTCCCTTAAAGGAAGAGGAGTAGCACTCTTGTCTGGACATCGAAACAGCCACTCGTGCA	180	
QY	181	GGAAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGCACTTAAATGACC	240	
DB	181	GGAAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGCACTTAAATGACC	240	
QY	241	ATTGCTCTGTCTCTGCTTCAGCTACTTAACTGACATGACTCTTTCAGATGTCAGA	300	
DB	241	ATTGCTCTGTCTCTGCTTCAGCTACTTAACTGACATGACTCTTTCAGATGTCAGA	300	

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QY 301 GACTGTTTCATGCTCATGCCCAAGCAGAAAGTAACAGGCTCCCTATGTATAGAAATGGAC 360
DB 301 GACTGTTTCATGCTCATGCCCAAGCAGAAAGTAACAGGCTCCCTATGTATAGAAATGGAC 360
QY 361 CAGGCAATCATGGATTAAGAACATCATACTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG 420
DB 361 CAGGCAATCATGGATTAAGAACATCATACTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG 420
QY 421 CTGGAGACACTAATACTACTTACAGGCTTTCACCGAAGAGGACGCTCGTTGGCGAATT 480
DB 421 CTGGAGACACTAATACTACTTACAGGCTTTCACCGAAGAGGACGCTCGTTGGCGAATT 480
QY 481 TCACCAATTCGCTTCTCTCCAGGACATCTAATGAGTGTCAAAATCGAATTTGGGTC 540
DB 481 TCACCAATTCGCTTCTCTCCAGGACATCTAATGAGTGTCAAAATCGAATTTGGGTC 540
QY 541 CTCATCGGAGACTTAATGGAATGATACGTTAGATCTCTGAACTCTACAGAGA 600
DB 541 CTCATCGGAGACTTAATGGAATGATACGTTAGATCTCTGAACTCTACAGAGA 600
QY 601 TTCGCTTGGAGAGAGTCAATGGAATGGAGACCTTCATTCCTCCCAAGCAGAAACGA 660
DB 601 TTCGCTTGGAGAGAGTCAATGGAATGGAGACCTTCATTCCTCCCAAGCAGAAACGA 660
QY 661 AAAATGGAGAGAACTTGGAGCCAGAAATT 690
DB 661 AAAATGGAGAGAACTTGGAGCCAGAAATT 690
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## RESULT 2

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US-09-506-286B-59
; Sequence 59, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 59
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-59
```

```
Query Match 100.0%; Score 690; DB 3; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.6e-212; Indels 0; Gaps 0;
Matches 690; Conservative 0; Mismatches 0;

QY 1 ATGGATTCACACATGTGTGACGTTTCAGGTAGACACTGTTTCTTTGGCATGTCCGAAA 60
DB 1 ATGGATTCACACATGTGTGACGTTTCAGGTAGACACTGTTTCTTTGGCATGTCCGAAA 60
QY 61 CGAATTCGAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCGAGACGAG 120
DB 61 CGAATTCGAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCGAGACGAG 120
QY 121 AAGTCCCTTAAAGAGGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180
DB 121 AAGTCCCTTAAAGAGGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180
QY 181 GGAAGCAGATAGTGAGAGCAGATTCTTGGAGAGGAGTAATCAGATGAGGCACTTAAATGACC 240
DB 181 GGAAGCAGATAGTGAGAGCAGATTCTTGGAGAGGAGTAATCAGATGAGGCACTTAAATGACC 240
```

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QY 241 ATTGCCTCTGTTCTCTTCCTTCAAGCAATGATCACTCTTGTAGATGATGTCGAAGA 300
DB 241 ATTGCCTCTGTTCTCTTCCTTCAAGCAATGATCACTCTTGTAGATGATGTCGAAGA 300
QY 301 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAACAGGCTCCCTATGTATAGAAATGGAC 360
DB 301 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAACAGGCTCCCTATGTATAGAAATGGAC 360
QY 361 CAGCAATCATGATTAAGAACATCATCTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG 420
DB 361 CAGCAATCATGATTAAGAACATCATCTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG 420
QY 421 CTGGAGACACTAATACTACTTACAGGCTTTCACCGAAGAGGACGCTCGTTGGCGAATT 480
DB 421 CTGGAGACACTAATACTACTTACAGGCTTTCACCGAAGAGGACGCTCGTTGGCGAATT 480
QY 481 TCACCAATTCGCTTCTCTCCAGGACATCTAATGAGTGTCAAAATCGAATTTGGGTC 540
DB 481 TCACCAATTCGCTTCTCTCCAGGACATCTAATGAGTGTCAAAATCGAATTTGGGTC 540
QY 541 CTCATCGGAGACTTAATGGAATGATACGTTAGATCTCTGAACTCTACAGAGA 600
DB 541 CTCATCGGAGACTTAATGGAATGATACGTTAGATCTCTGAACTCTACAGAGA 600
QY 601 TTCGCTTGGAGAGAGTCAATGGAATGGAGACCTTCATTCCTCCCAAGCAGAAACGA 660
DB 601 TTCGCTTGGAGAGAGTCAATGGAATGGAGACCTTCATTCCTCCCAAGCAGAAACGA 660
QY 661 AAAATGGAGAGAACTTGGAGCCAGAAATT 690
DB 661 AAAATGGAGAGAACTTGGAGCCAGAAATT 690
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## RESULT 3

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US-10-065-133A-52
; Sequence 52, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 52
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-52
```

```
Query Match 100.0%; Score 690; DB 3; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.6e-212; Indels 0; Gaps 0;
Matches 690; Conservative 0; Mismatches 0;

QY 1 ATGGATTCACACATGTGTGACGTTTCAGGTAGACACTGTTTCTTTGGCATGTCCGAAA 60
DB 1 ATGGATTCACACATGTGTGACGTTTCAGGTAGACACTGTTTCTTTGGCATGTCCGAAA 60
QY 61 CGAATTCGAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCGAGACGAG 120
DB 61 CGAATTCGAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCGAGACGAG 120
QY 121 AAGTCCCTTAAAGAGGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180
DB 121 AAGTCCCTTAAAGAGGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180
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QY 181 GGAAGCAGATAGTGGAGCAGATTTCTGGAGAGGAGATCAGATGAGGACCTTAAATGACC 240  
DB 181 GGAAGCAGATAGTGGAGCAGATTTCTGGAGAGGAGATCAGATGAGGACCTTAAATGACC 240  
QY 241 ATTGCCTCTGTTCTGCTTCAACGCTACTTAACGATGATCTTTGATGAGATGTCAAGA 300  
DB 241 ATTGCCTCTGTTCTGCTTCAACGCTACTTAACGATGATCTTTGATGAGATGTCAAGA 300  
QY 301 GACTGTTCAATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAAGATGGAC 360  
DB 301 GACTGTTCAATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAAGATGGAC 360  
QY 361 CAGGCAATCATGGATAAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTGGAAAGG 420  
DB 361 CAGGCAATCATGGATAAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTGGAAAGG 420  
QY 421 CTGGAGACACTAACTACTTACGAGCTTTCCCGAAGAGGAGCAGCTGTTGGCGAAAT 480  
DB 421 CTGGAGACACTAACTACTTACGAGCTTTCCCGAAGAGGAGCAGCTGTTGGCGAAAT 480  
QY 481 TCACCATTCGCTTCTCTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGGTC 540  
DB 481 TCACCATTCGCTTCTCTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGGTC 540  
QY 541 CTCATCGGAGACTTAATGGAATGATATACGGTTAGAACTCTTGAACTCTACAGAGA 600  
DB 541 CTCATCGGAGACTTAATGGAATGATATACGGTTAGAACTCTTGAACTCTACAGAGA 600  
QY 601 TTGCTTGGAGAGCAGTCAATGAGAAATGAGAGCTTCATTCCTCCCAAAGCAGAAACGA 660  
DB 601 TTGCTTGGAGAGCAGTCAATGAGAAATGAGAGCTTCATTCCTCCCAAAGCAGAAACGA 660  
QY 661 AAAATGGAGAGCAAAATTTGAGCCAGAAATTT 690  
DB 661 AAAATGGAGAGCAAAATTTGAGCCAGAAATTT 690

## RESULT 4

US-10-065-133A-59  
; Sequence 59, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; PRIOR FILING DATE: 2002-12-10  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 59  
; LENGTH: 690  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-10-065-133A-59

Query Match 100.0%; Score 690; DB 3; Length 690;  
Best Local Similarity 100.0%; Pred. No. 1.6e-212;  
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTTCAACACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAAA 60  
DB 1 ATGGATTTCAACACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAAA 60  
QY 61 CGATTTGAGACCAAGAACTGGGTGATGCCCCATTCCTGACGGCTTCGCGAGACGAG 120  
DB 61 CGATTTGAGACCAAGAACTGGGTGATGCCCCATTCCTGACGGCTTCGCGAGACGAG 120  
QY 121 AGTTCCTTAAAGAGAGGAGTAGACTCTTGTGCTGGAGACATCGAAGACGACCACTCGTGCA 180

DB 121 AAGTTCCTTAAAGAGAGGAGTAGACTCTTGTGCTGGAGACATCGAAGACGACCACTCGTGCA 180  
QY 181 GGAAGCAGATAGTGGAGCAGATTTCTGGAGAGGAGATCAGATGAGGACCTTAAATGACC 240  
DB 181 GGAAGCAGATAGTGGAGCAGATTTCTGGAGAGGAGATCAGATGAGGACCTTAAATGACC 240  
QY 241 ATTGCCTCTGTTCTGCTTCAACGCTACTTAACGATGATCTTTGATGAGATGTCAAGA 300  
DB 241 ATTGCCTCTGTTCTGCTTCAACGCTACTTAACGATGATCTTTGATGAGATGTCAAGA 300  
QY 301 GACTGTTCAATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAAGATGGAC 360  
DB 301 GACTGTTCAATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAAGATGGAC 360  
QY 361 CAGGCAATCATGGATAAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTGGAAAGG 420  
DB 361 CAGGCAATCATGGATAAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTGGAAAGG 420  
QY 421 CTGGAGACACTAACTACTTACGAGCTTTCCCGAAGAGGAGCAGCTGTTGGCGAAAT 480  
DB 421 CTGGAGACACTAACTACTTACGAGCTTTCCCGAAGAGGAGCAGCTGTTGGCGAAAT 480  
QY 481 TCACCATTCGCTTCTCTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGGTC 540  
DB 481 TCACCATTCGCTTCTCTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGGTC 540  
QY 541 CTCATCGGAGACTTAATGGAATGATATACGGTTAGAACTCTTGAACTCTACAGAGA 600  
DB 541 CTCATCGGAGACTTAATGGAATGATATACGGTTAGAACTCTTGAACTCTACAGAGA 600  
QY 601 TTGCTTGGAGAGCAGTCAATGAGAAATGAGAGCTTCATTCCTCCCAAAGCAGAAACGA 660  
DB 601 TTGCTTGGAGAGCAGTCAATGAGAAATGAGAGCTTCATTCCTCCCAAAGCAGAAACGA 660  
QY 661 AAAATGGAGAGCAAAATTTGAGCCAGAAATTT 690  
DB 661 AAAATGGAGAGCAAAATTTGAGCCAGAAATTT 690

## RESULT 5

US-09-506-286B-53  
; Sequence 53, Application US/09506286B  
; Patent No. 6482414  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2  
; CURRENT APPLICATION NUMBER: US/09/506,286B  
; CURRENT FILING DATE: 2000-02-16  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 53  
; LENGTH: 888  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
US-09-506-286B-53

Query Match 100.0%; Score 690; DB 3; Length 888;  
Best Local Similarity 100.0%; Pred. No. 1.9e-212;  
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGATTTCAACACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAAA 60  
DB 25 ATGGATTTCAACACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAAA 84  
QY 61 CGATTTGAGACCAAGAACTGGGTGATGCCCCATTCCTTGGACGGCTTCGCGAGACGAG 120







APPLICANT: Dowling, Patricia W.  
APPLICANT: Youngner, Julius S.  
TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
FILE REFERENCE: EQ-1-C2-1  
CURRENT APPLICATION NUMBER: US/10/065,133A  
CURRENT FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: PCT/US99/18583  
PRIOR FILING DATE: 1999-08-12  
PRIOR APPLICATION NUMBER: 09/133,921  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 50  
LENGTH: 891  
TYPE: DNA  
ORGANISM: Equine influenza virus H3N8  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (27)..(716)  
OTHER INFORMATION:  
US-10-065-133A-50

Query Match 100.0%; Score 690; DB 3; Length 891;  
Best Local Similarity 100.0%; Pred. No. 1.9e-212; Mismatches 0; Indels 0; Gaps 0;  
Matches 690; Conservative 0; Indels 0; Gaps 0;

QY 1 ATGGATTCCAAACACTGTCTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAA 60  
DB 27 ATGGATTCCAAACACTGTCTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAA 86  
QY 61 CGATTTCGAGACCAAGAACTGGGTGATGCCCATTTCTTGGCCGCTTCCGCGAGACGAG 120  
DB 87 CGATTTCGAGACCAAGAACTGGGTGATGCCCATTTCTTGGCCGCTTCCGCGAGACGAG 146  
QY 121 AAGTCCCTTAAAGAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCTGTGCA 180  
DB 147 AAGTCCCTTAAAGAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCTGTGCA 206  
QY 181 GGAAGCAGATAGTGGAGCAGATTTCGGAAGAGGATCAGATGAGGCACCTTAAATGACC 240  
DB 207 GGAAGCAGATAGTGGAGCAGATTTCGGAAGAGGATCAGATGAGGCACCTTAAATGACC 266  
QY 241 ATTGCTCTCTTCTGCTTCCAGCTTAACTGATGATGATGATGATGATGATGATGATGATGAT 300  
DB 267 ATTGCTCTCTTCTGCTTCCAGCTTAACTGATGATGATGATGATGATGATGATGATGATGAT 326  
QY 301 GACTGGTTCATGCTCATGCCAGAGAAAGTAAAGGCTCCCTATGATGATGATGATGATGATGATGAT 360  
DB 327 GACTGGTTCATGCTCATGCCAGAGAAAGTAAAGGCTCCCTATGATGATGATGATGATGATGATGAT 386  
QY 361 CAGGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
DB 387 CAGGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 446  
QY 421 CTGGAGACACTAATCTACTTCTAGAGCCCTTCAACGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
DB 447 CTGGAGACACTAATCTACTTCTAGAGCCCTTCAACGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 506  
QY 481 TCACCATTCGCTTCTCTTCCAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
DB 507 TCACCATTCGCTTCTCTTCCAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 566  
QY 541 CTCATCGAGAGGACTTAAATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
DB 567 CTCATCGAGAGGACTTAAATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 626  
QY 601 TTCGCTTGGAGAGGAGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
DB 627 TTCGCTTGGAGAGGAGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 686  
QY 661 AAAATGGAGAGAACTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 690  
DB 687 AAAATGGAGAGAACTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 716

PRIOR APPLICATION NUMBER: 09/133,921  
PRIOR FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: PCT/US99/18583  
PRIOR FILING DATE: 1999-08-12  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 50  
LENGTH: 891  
TYPE: DNA  
ORGANISM: Equine influenza virus H3N8  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (27)..(716)  
US-09-506-286B-50

Query Match 100.0%; Score 690; DB 3; Length 891;  
Best Local Similarity 100.0%; Pred. No. 1.9e-212; Mismatches 0; Indels 0; Gaps 0;  
Matches 690; Conservative 0; Indels 0; Gaps 0;

QY 1 ATGGATTCCAAACACTGTCTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAA 60  
DB 27 ATGGATTCCAAACACTGTCTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAA 86  
QY 61 CGATTTCGAGACCAAGAACTGGGTGATGCCCATTTCTTGGCCGCTTCCGCGAGACGAG 120  
DB 87 CGATTTCGAGACCAAGAACTGGGTGATGCCCATTTCTTGGCCGCTTCCGCGAGACGAG 146  
QY 121 AAGTCCCTTAAAGAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCTGTGCA 180  
DB 147 AAGTCCCTTAAAGAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCTGTGCA 206  
QY 181 GGAAGCAGATAGTGGAGCAGATTTCGGAAGAGGATCAGATGAGGCACCTTAAATGACC 240  
DB 207 GGAAGCAGATAGTGGAGCAGATTTCGGAAGAGGATCAGATGAGGCACCTTAAATGACC 266  
QY 241 ATTGCTCTCTTCTGCTTCCAGCTTAACTGATGATGATGATGATGATGATGATGATGATGATGAT 300  
DB 267 ATTGCTCTCTTCTGCTTCCAGCTTAACTGATGATGATGATGATGATGATGATGATGATGATGAT 326  
QY 301 GACTGGTTCATGCTCATGCCAGAGAAAGTAAAGGCTCCCTATGATGATGATGATGATGATGATGATGAT 360  
DB 327 GACTGGTTCATGCTCATGCCAGAGAAAGTAAAGGCTCCCTATGATGATGATGATGATGATGATGATGAT 386  
QY 361 CAGGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
DB 387 CAGGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 446  
QY 421 CTGGAGACACTAATCTACTTCTAGAGCCCTTCAACGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
DB 447 CTGGAGACACTAATCTACTTCTAGAGCCCTTCAACGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 506  
QY 481 TCACCATTCGCTTCTCTTCCAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
DB 507 TCACCATTCGCTTCTCTTCCAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 566  
QY 541 CTCATCGAGAGGACTTAAATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
DB 567 CTCATCGAGAGGACTTAAATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 626  
QY 601 TTCGCTTGGAGAGGAGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
DB 627 TTCGCTTGGAGAGGAGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 686  
QY 661 AAAATGGAGAGAACTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 690  
DB 687 AAAATGGAGAGAACTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 716

RESULT 10  
US-10-065-133A-50  
; Sequence 50, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:

## RESULT 11

US-10-204-664A-6  
; Sequence 6, Application US/10204664A  
; Patent No. 6800288  
; GENERAL INFORMATION:  
; APPLICANT: FERKO, Boris  
; APPLICANT: EGOROV, Andre  
; APPLICANT: VOGLAUER, Regina  
; TITLE OF INVENTION: Recombinant Influenza A Viruses  
; FILE REFERENCE: 113529  
; CURRENT APPLICATION NUMBER: US/10/204,664A  
; PRIOR FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: EP 00104338.9  
; PRIOR FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 6  
; LENGTH: 906  
; TYPE: DNA  
; ORGANISM: Influenza A virus /PR8NS38

## US-10-204-664A-6

Query Match 77.2%; Score 532.4; DB 3; Length 906;  
Best Local Similarity 87.0%; Pred. No. 1.6e-161;  
Matches 614; Conservative 0; Mismatches 76; Indels 16; Gaps 2;

QY	1	ATGGATTCCAAACACATGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAA	60
DB	27	ATGGATCCAAACACATGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAA	86
QY	61	CGATTTGCAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCCCGAG	115
DB	87	CGAGTTGCAGACCAAGAACTAGGTGATGCCCATTCCTTTGATCGGCTTCCCGAGTGAAT	146
QY	116	-----ACCAGAAGTCCCTAAAGAGAGAGTGTAGCACTCTTGCTTGGACATCGAA	165
DB	147	AACATGCTGATCAGAAATCCCTAAGAGAGAGGCGACACCTCGGTCTGCACATCGAG	206
QY	166	ACAGCCACTCGTGCAGAGAGAGAGATGTGGAGCAGATCTGTGGAGAGAGATCATGAG	225
DB	207	ACAGCCACAGTGTCTGAGAGAGAGATGTGGAGCAGATCTGTGGAGAGAGATCATGAG	266
QY	226	GCATTTAAATGACCAATTCCTCTGTTCTGCTTCACTGCTTCACTTAACTGACATGACTTT	285
DB	267	GCATTTAAATGACCAATTCCTCTGTTCTGCTTCACTGCTTCACTTAACTGACATGACTTT	326
QY	286	GATGAGATGTCAGAGACTGTCTCATGCTCATGCCAAGCAGAAAGTAAACAGGCTCCCTA	345
DB	327	GAGGAAATGTCAGAGACTGTCTCATGCTCATGCCAAGCAGAAAGTAAACAGGCTCCCTT	386
QY	346	TGTATGAATGAGACCGGCAATCATGGA-TAAGAAATCATACTTAAAGCAAACTTTAG	404
DB	387	TGTATCAGATGAGACCGGCAATCATGGA-TAAGAAATCATACTTAAAGCAAACTTTAG	446
QY	405	TGTATTTTCGAAGGCTGGAGACACTTAATCTACTTACCTTACCGGCTTTTACCGGAGAGG	464
DB	447	TGTATTTTCGAAGGCTGGAGACACTTAATCTACTTACCTTACCGGCTTTTACCGGAGAGG	506
QY	465	AGTCGTTGGCAAAATTTTCAACATTCGCTTCTTCCAGGACATCAATGAGAGTGTCAA	524
DB	507	AAATGTTGGCAAAATTTTCAACATTCGCTTCTTCCAGGACATCAATGAGAGTGTCAA	566
QY	525	AAATGCAATTTGGGTCCTCATCGAGAGACTTAAATGGAATGATTAATACGGTTAGATCTC	584
DB	567	AAATGCAATTTGGGTCCTCATCGAGAGACTTAAATGGAATGATTAATACGGTTAGATCTC	626
QY	585	TGAACCTCTACAGAGATTCGCTTGGAGAGAGAGTGTGAGATGGGAGACCTTCATTC	644
DB	627	TGAACCTCTACAGAGATTCGCTTGGAGAGAGAGTGTGAGATGGGAGACCTTCATTC	686
QY	645	TCCAAAGCAGAAACGAAATGGAGAGACAAATTCAGGCCAGAGTT	690

Db 687 TCCAAACAGAAACGAAATGCGGGAACAATTAGGTGAGAAGTT 732

## RESULT 12

US-09-506-286B-56  
; Sequence 56, Application US/09506286B  
; Patent No. 6482414  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; APPLICANT: The University of Pittsburgh, of the Commonwealth  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2  
; CURRENT APPLICATION NUMBER: US/09/506,286B  
; CURRENT FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 56  
; LENGTH: 293  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8

Query Match 42.2%; Score 291.4; DB 3; Length 293;  
Best Local Similarity 99.7%; Pred. No. 6.7e-84;  
Matches 292; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	398	ACTTTAGTGTGATTTTCGAAAGCTGGAGACACTAACTACTTACAGGCTTCCACCGAAG	457
DB	1	ACTTTAGTGTGATTTTCGAAAGCTGGAGACACTAACTACTTACAGGCTTCCACCGAAG	60
QY	458	AAGGAGCAGTGTGGCGAAATTCACCATTCGCTTCCAGGACATCTAATGAGG	517
DB	61	AAGGAGCAGTGTGGCGAAATTCACCATTCGCTTCCAGGACATCTAATGAGG	120
QY	518	ATGTCAAAATGCAATTTGGGCTTCATCGGAGACTTAAATGGAATGATATACGGTTA	577
DB	121	ATGTCAAAATGCAATTTGGGCTTCATCGGAGACTTAAATGGAATGATATACGGTTA	180
QY	578	GAATCTCTGAAACTCTACAGAGATTCGCTTCGAGAGACAGTCAATGAGATGGAGACCTT	637
DB	181	GAATCTCTGAAACTCTACAGAGATTCGCTTCGAGAGACAGTCAATGAGATGGAGACCTT	240
QY	638	CATTCCCTCCAAAGCAGAAACGAAATGGAGAGAAACAATTCAGGCCAGAGTT	690
DB	241	CATTCCCTCCAAAGCAGAAACGAAATGGAGAGAAACAATTCAGGCCAGAGTT	293

## RESULT 13

US-10-065-133A-56  
; Sequence 56, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; APPLICANT: The University of Pittsburgh, of the Commonwealth  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 56  
; LENGTH: 293  
; TYPE: DNA

; ORGANISM: Equine influenza virus H3N8  
US-10-065-133A-56  
Query Match 42.2%; Score 291.4; DB 3; Length 293;  
Best Local Similarity 99.7%; Pred. No. 6.7e-84;  
Matches 292; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 398 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACATAAATACTACTTAGAGCCTTCACCGAAG 457  
Db 1 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACATAAATACTACTTAGAGCCTTCACCGAAG 60  
Qy 458 AAGGAGCAGTGGTGGGCAATTTTACCAATTCGCTTCTTCAGGACATATAATGAGG 517  
Db 61 AAGGAGCAGTGGTGGGCAATTTTACCAATTCGCTTCTTCAGGACATATAATGAGG 120  
Qy 518 ATGTCAAAAATGCAATTTGGGCTCTCATCGGAGACTTAAATGGAATGATATACGGTTA 577  
Db 121 ATGTCAAAAATGCAATTTGGGCTCTCATCGGAGACTTAAATGGAATGATATACGGTTA 180  
Qy 578 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 637  
Db 181 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 240  
Qy 638 CATTCCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCGAGCAGAGTT 690  
Db 241 CATTCCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCGAGCAGAGTT 293

RESULT 14  
US-09-506-286B-54  
; Sequence 54, Application US/09506286B  
; Patent No. 6482414  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; APPLICANT: The University of Pittsburgh, of the Commonwealth  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2  
; CURRENT APPLICATION NUMBER: US/09/506,286B  
; CURRENT FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 54  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3)..(293)  
US-09-506-286B-54

Query Match 42.2%; Score 291.4; DB 3; Length 468;  
Best Local Similarity 99.7%; Pred. No. 8.6e-84;  
Matches 292; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 398 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACATAAATACTACTTAGAGCCTTCACCGAAG 457  
Db 1 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACATAAATACTACTTAGAGCCTTCACCGAAG 60  
Qy 458 AAGGAGCAGTGGTGGGCAATTTTACCAATTCGCTTCTTCAGGACATATAATGAGG 517  
Db 61 AAGGAGCAGTGGTGGGCAATTTTACCAATTCGCTTCTTCAGGACATATAATGAGG 120  
Qy 518 ATGTCAAAAATGCAATTTGGGCTCTCATCGGAGACTTAAATGGAATGATATACGGTTA 577  
Db 121 ATGTCAAAAATGCAATTTGGGCTCTCATCGGAGACTTAAATGGAATGATATACGGTTA 180  
Qy 578 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 637

Db 181 GAATCTCTGAAACTCTACAGAGATTCGCTTCGAGAGACAGTCATGAGATGGAGACCTT 240  
Qy 638 CATTCCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCGAGCAGAGTT 690  
Db 241 CATTCCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCGAGCAGAGTT 293  
RESULT 15  
US-10-065-133A-54  
; Sequence 54, Application US/10065133A  
; Patent No. 6685946  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; APPLICANT: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 54  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Equine influenza virus H3N8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3)..(293)  
; OTHER INFORMATION:  
US-10-065-133A-54

Query Match 42.2%; Score 291.4; DB 3; Length 468;  
Best Local Similarity 99.7%; Pred. No. 8.6e-84;  
Matches 292; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 398 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACATAAATACTACTTAGAGCCTTCACCGAAG 457  
Db 1 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACATAAATACTACTTAGAGCCTTCACCGAAG 60  
Qy 458 AAGGAGCAGTGGTGGGCAATTTTACCAATTCGCTTCTTCAGGACATATAATGAGG 517  
Db 61 AAGGAGCAGTGGTGGGCAATTTTACCAATTCGCTTCTTCAGGACATATAATGAGG 120  
Qy 518 ATGTCAAAAATGCAATTTGGGCTCTCATCGGAGACTTAAATGGAATGATATACGGTTA 577  
Db 121 ATGTCAAAAATGCAATTTGGGCTCTCATCGGAGACTTAAATGGAATGATATACGGTTA 180  
Qy 578 GAATCTCTGAAACTCTACAGAGATTCGCTTCGAGAGACAGTCATGAGATGGAGACCTT 637  
Db 181 GAATCTCTGAAACTCTACAGAGATTCGCTTCGAGAGACAGTCATGAGATGGAGACCTT 240  
Qy 638 CATTCCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCGAGCAGAGTT 690  
Db 241 CATTCCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCGAGCAGAGTT 293

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Job time : 231.875 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 00:06:39 : Search time 3487.17 Seconds  
(without alignments)  
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Title:  
Perfect score: 690  
Sequence: 1 atggtatccaacactgtgtc.....gaacaattgagccagaagtt 690

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues  
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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EST:  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_hic.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_est7.\*  
9: gb\_gsa1.\*  
10: gb\_gsa2.\*  
11: gb\_gsa3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	6.4	509	3	BM952076
2	40.8	5.9	544	3	BI885258
3	40.6	5.9	763	2	BE785748
4	40.4	5.9	474	9	AQ308098
5	40.4	5.9	593	7	CK336719
6	39.2	5.7	789	3	BI434619
7	38.4	5.6	981	10	CNS0064P
8	38	5.5	645	2	BE436394
9	38	5.5	689	2	BE436400
10	38	5.5	703	1	AJ784580
11	38	5.5	718	1	AJ831883
12	38	5.5	720	3	BM534953
13	38	5.5	724	2	BGI29051
14	38	5.5	775	7	CV470467
15	38	5.5	777	3	BM413146
16	38	5.5	799	3	BM535551
17	38	5.5	865	8	DN22619
18	37.8	5.3	484	3	BP883758
19	37.8	5.3	553	3	BM869534
20	37.8	5.5	745	1	AW037484
21	37.8	5.5	885	10	CG789515
22	37.6	5.4	1101	10	CNS0021J

23	37.6	5.4	1101	10	CNS00KK2
24	37.4	5.4	767	9	AZ242813
25	37.2	5.4	1185	6	CA462358
26	37	5.4	580	10	CL929673
27	37	5.4	824	6	CB634856
28	36.8	5.3	775	10	BI187584
29	36.8	5.3	985	10	CNS02K3U
30	36.6	5.3	485	2	BF711497
31	36.6	5.3	799	10	DU039001
32	36.4	5.3	505	9	AZ173148
33	36.4	5.3	635	3	BM360828
34	36.4	5.3	665	1	AW218935
35	36.2	5.2	384	7	CO497058
36	36.2	5.2	587	8	DN756261
37	36.2	5.2	725	10	CZ421104
38	36.2	5.2	744	5	BM716173
39	36.2	5.2	845	7	CO090945
40	36.2	5.2	848	7	CO02083
41	36.2	5.2	870	10	CG847516
42	36.2	5.2	871	7	CO125308
43	36.2	5.2	882	7	CO099059
44	36.2	5.2	900	7	CO124880
45	36.2	5.2	916	10	CG848245

## ALIGNMENTS

RESULT 1  
BM952076 509 bp mRNA linear EST 14-MAR-2002  
LOCUS rc55a04.y1 Meloidogyne hapla egg pAMP1 v1 Meloidogyne hapla cDNA 5'  
DEFINITION T16H12.4 IN CHROMOSOME III. ; mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BM952076  
BM952076.1 GI:19435666  
EST  
Meloidogyne hapla  
Meloidogyne hapla  
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchinae;  
Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.

REFERENCE  
AUTHORS

McCartner, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,  
Wyllie, I., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,  
Bowers, J., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
Teagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,  
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCann, R., Waterston, R. and Wilson, R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
The library was constructed by Claire Murphy and Dr. James McCarter  
at Washington University, St. Louis. DNA Sequencing by: Washington  
University Genome Sequencing Center  
Seq primer: -408P from Gibco  
High quality sequence stop: 400.  
Location/Qualifiers  
1: 509  
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/dev\_stage="parasitic adult females"  
/lab\_host="DH10B"  
/clone\_lib="Meloidogyne hapla egg pAMP1 v1"  
/note="Vector: pAMP1 (Gibco); Site: 1: NotI; Site 2: Sall;  
The library was constructed by Claire Murphy and Dr. James

TITLE  
JOURNAL  
COMMENT

FEATURES  
source



/notes="Organ: lung; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: oligo dt.  
Average insert size 1.8 kb. Library constructed by Life  
Technologies."

## ORIGIN

Query Match 5.9%; Score 40.6; DB 2; Length 763;  
Best Local Similarity 52.0%; Pred. No. 1.8;  
Matches 91; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 290 AGATGTCAGAGACTGTTTCATGCTCATGCCCAAGCAGAAAGTACAGGCTCCCTATGTA 349  
DB 392 AGCTGTCAATATAATATAATATGCTTTCTTAAAAAAGTATTTTACAGACAGATAGTGA 333

QY 350 TAAGATGGACAGGCAATCATGATGAAGACATCATCTTAAGCAAACTTTAGTGTA 409  
DB 332 TATACATTTGTTCACTTGTGATCTGGGCAAAAGAAAGCTAAACACAGCTTAAGTGTA 273

QY 410 TTTTCGAAAGCTGGAGACACTAATCTACTTAGAGCCTTACCCGACAGAGGAC 464  
DB 272 TATATAAAGATGATACATAAATGACGTTTAAACCTGCTAGAAATGAGC 218

## RESULT 4

LOCUS AQ308098 474 bp DNA linear GSS 22-DEC-1998  
DEFINITION CITBI-EI-2525L17.TF CITBI-EI Homo sapiens genomic clone 2525L17,  
genomic survey sequence.  
ACCESSION AQ308098  
VERSION AQ308098.1 GI:4040450  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 474)  
ADAMS M.D., ROUNSELEY S.D., ZHAO S., BASS S., LINHER K., GOLDEN K.,  
BERRY K., GRANGER D., SUH E., WIBLE C., SHIZUYA H., SIMON M. and  
VENTER J.C.  
Use of a random human BAC End Sequence Database for Sequence-Ready  
Map Building  
Unpublished (1998)  
CONTACT: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0208  
Fax: 301 838 0208  
Email: hwe@cigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:  
http://www.cigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13-21  
Class: BAC ends.

## JOURNAL

## COMMENT

## FEATURES

## source

## Location/Qualifiers

1. 474  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="2525L17"  
/sex="male"  
/cell\_type="sperm"  
/clone\_lib="CITBI-EI"  
/notes="Vector: pBelOBAC11; Site\_1: EcoRI; Site\_2: EcoRI;  
CalTech Human BAC Library D"

## ORIGIN

Query Match 5.9%; Score 40.4; DB 9; Length 474;  
Best Local Similarity 58.2%; Pred. No. 1.8;  
Matches 71; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 506 ATACTATGAGGTGTCAAAATGCAATGGGTCTCTCATCGGAGGACTTAATGGAATG 565

DB 142 ATACGATAGTCAAGTAAAAATGCAATTTGACATCTTCAACAGAAATTTGATCAACAG 201  
QY 566 ATATACGGTTAGAACTCTGAAACTCTACAGAGATTGGCTTGGAGAGCACTCATGAGA 625  
DB 202 AAGAAAGAAATCAGGCTATTTGAAAATGCACAGAGAGAAAAAGGAAAGCAACACGAGA 261  
QY 626 AT 627  
DB 262 AT 263

## RESULT 5

LOCUS CK336719/c 593 bp mRNA linear EST 22-DEC-2003  
DEFINITION C0254D07-3 NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long) Mus  
musculus cDNA clone NIA:C0254D07 IMAGE:30015786 3', mRNA sequence.  
ACCESSION CK336719  
VERSION CK336719.1 GI:40292332  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Murioidea; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 593)  
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.  
Construction of long-transcript enriched cDNA libraries from  
submicrogram amounts of total RNAs by a universal PCR amplification  
method  
Genome Res. 11 (9), 1553-1558 (2001)  
11544199  
CONTACT: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@gsun.grc.nia.nih.gov  
Phone: C0254 row: D column: 07  
Seq primer: -21M13 Forward  
High quality sequence stop: 593  
POLYA=Yes

## FEATURES

## source

## Location/Qualifiers

1. 593  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="NIA:C0254D07 IMAGE:30015786"  
/tissue\_type="whole embryo including extraembryonic  
tissues at 7.5-days postcoitum"  
/dev\_stage="7.5-days postcoitum"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library  
(Long)"  
/note="Vector: pSPORT1 (Invitrogen); Site\_1: SalI; Site\_2:  
NotI; Mouse cDNA project by the Laboratory of Genetics,  
National Institute on Aging (NIA), Intramural Research  
Program, NIH (http://gsun.grc.nia.nih.gov/cDNA). This is  
a long-transcript enriched cDNA library (Ref. Genome Res.  
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were  
extracted from a pool of four embryos at 7.5-days  
postcoitum. Double-stranded cDNAs were synthesized with an  
Oligo(dT) primer (Invitrogen):  
5'-GGATCTCTTAGTCGGAGCGCGCCCTTTTTTTTTT-3' from  
7 ug of total RNA, treated with T4 DNA polymerase, and  
purified by ethanol-precipitation. The cDNAs were ligated  
to Lox-linker L1-SalI, purified by phenol/chloroform and  
separated from free linker by centrifugation. Then, the  
cDNAs were amplified by long-range high fidelity PCR using  
Ex taq polymerase (Takara) with a primer SalI-S. The  
products were purified by phenol/chloroform and Centricon  
100. The cDNAs were digested with SalI and NotI enzymes







ORGANISM Lycopersicon esculentum var. cerasiforme  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.  
1 (bases 1 to 703)  
Lemaire-Chamley, M., Petit, J., Garcia, V., Baldet, P., Fagard, M.,  
Germain, V., Just, D. and Rothan, C.  
Gene expression is spatially controlled in developing tomato fruit  
Unpublished (2004)  
Contact: Garcia V  
Physiologie et Biotechnologie Vegetales  
INRA  
71 avenue E. Bourleaux, Villenave d'Ornon, 33883, FRANCE.  
Location/Qualifiers  
1..703  
/organism="Lycopersicon esculentum var. cerasiforme"  
/mol\_type="mRNA"  
/cultivar="West Virginia 106"  
/db\_xref="taxon:195583"  
/clone="LE08CB07"  
/tissue\_type="fruit"  
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/clone\_lib="Lycopersicon esculentum var. cerasiforme fruit  
8 days post anthesis"

ORIGIN  
Query Match 5.5%; Score 38; DB 1; Length 703;  
Best Local Similarity 60.8%; Pred. No. 10;  
Matches 62; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 144 CACTCTTGCTCGACATCGAAACAGCCACTCGTCAGGAAAGCAGATAGTGAGCAGAT 203  
|||  
DB 282 CAAGCCTAGTTTGGACAAAGAAAGACCCCATGCGAGGAATATGATATGATGAAGAA 341  
|||

QY 204 TCTGGAAGAGGAATCAGATGAGGCACCTTAAATGACCATTCG 245  
|||  
DB 342 CATGTATGAGGACGGTGATGAGGAATGAAGAACAATTGC 383  
|||

RESULT 11  
AJ831883/c  
LOCUS  
DEFINITION  
AJ831883 Lycopersicon esculentum var. cerasiforme fruit 8 days post  
anthesis Lycopersicon esculentum var. cerasiforme cDNA clone  
LE08CB04, mRNA sequence.  
ACCESSION  
AJ831883.1 GI:52619144  
KEYWORDS  
EST.  
SOURCE  
Lycopersicon esculentum var. cerasiforme (Solanum lycopersicum var.  
cerasiforme)  
ORGANISM  
Lycopersicon esculentum var. cerasiforme  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.  
1 (bases 1 to 718)  
Lemaire-Chamley, M., Petit, J., Garcia, V. and Rothan, C.  
Transcriptional profiling of fruit tissues reveals novel features  
of early fruit development in tomato  
Unpublished (2004)  
Contact: Garcia V  
Physiologie et Biotechnologie Vegetales  
INRA  
71 avenue E. Bourleaux, Villenave d'Ornon, 33883, FRANCE.  
Location/Qualifiers  
1..718  
/organism="Lycopersicon esculentum var. cerasiforme"  
/mol\_type="mRNA"  
/cultivar="West Virginia 106"  
/db\_xref="taxon:195583"  
/clone="LE08CB04"  
/tissue\_type="fruit"  
/dev\_stage="8 days post anthesis"  
/clone\_lib="Lycopersicon esculentum var. cerasiforme fruit  
8 days post anthesis"

ORIGIN  
Query Match 5.5%; Score 38; DB 1; Length 718;  
Best Local Similarity 60.8%; Pred. No. 11;  
Matches 62; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 144 CACTCTTGCTCGACATCGAAACAGCCACTCGTCAGGAAAGCAGATAGTGAGCAGAT 203  
|||  
DB 422 CAAGCCTAGTTTGGACAAAGAAAGACCCCATGCGAGGAATATGATATGATGAAGAA 363  
|||

QY 204 TCTGGAAGAGGAATCAGATGAGGCACCTTAAATGACCATTCG 245  
|||  
DB 362 CATGTATGAGGACGGTGATGAGGAATGAAGAACAATTGC 321  
|||

RESULT 12  
BM534953/c  
LOCUS  
DEFINITION  
BM534953  
EST.  
BM534953.1 GI:18813212  
KEYWORDS  
SOURCE  
Lycopersicon esculentum (Solanum lycopersicum)  
ORGANISM  
Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.  
1 (bases 1 to 720)  
Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A.,  
Tsai, J., Bougri, O., Kirkness, E., Utecht, T., Van Aken, S.,  
Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and  
Giovannoni, J.  
Generation of ESTs from tomato fruit tissue, breaker stage (2002)  
Unpublished (2002)  
Contact: CUGI  
Clemson University  
Clemson University Genomics Institute  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
This clone is available through the Clemson University Genomics  
Institute  
Seq primer: T3.  
Location/Qualifiers  
1..720  
/organism="Lycopersicon esculentum"  
/mol\_type="mRNA"  
/cultivar="TA496"  
/db\_xref="taxon:4081"  
/clone="CLEG64E13"  
/tissue\_type="Pericarp"  
/dev\_stage="breaker"  
/lab\_host="SOLR"  
/clone\_lib="tomato breaker fruit"  
/notes="Vector: pBluescriptSKmCquadapt; Site 1: EcoRI;  
Site 2: XhoI; supplier: Boyce Thompson Institute;  
sequencing: The Institute for Genomic Research. Fruit  
were harvested at the breaker stage (first sign of  
lycopene accumulation on the blossom end of fruit). Fruit  
were cut in half and the seeds and locules were discarded  
prior to freezing the pericarp."

FEATURES  
source  
1..720  
Location/Qualifiers  
1..720  
/organism="Lycopersicon esculentum"  
/mol\_type="mRNA"  
/cultivar="TA496"  
/db\_xref="taxon:4081"  
/clone="CLEG64E13"  
/tissue\_type="Pericarp"  
/dev\_stage="breaker"  
/lab\_host="SOLR"  
/clone\_lib="tomato breaker fruit"  
/notes="Vector: pBluescriptSKmCquadapt; Site 1: EcoRI;  
Site 2: XhoI; supplier: Boyce Thompson Institute;  
sequencing: The Institute for Genomic Research. Fruit  
were harvested at the breaker stage (first sign of  
lycopene accumulation on the blossom end of fruit). Fruit  
were cut in half and the seeds and locules were discarded  
prior to freezing the pericarp."

ORIGIN  
Query Match 5.5%; Score 38; DB 3; Length 720;  
Best Local Similarity 60.8%; Pred. No. 11;  
Matches 62; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 144 CACTCTTGCTCGACATCGAAACAGCCACTCGTCAGGAAAGCAGATAGTGAGCAGAT 203  
|||  
DB 293 CAAGCCTAGTTTGGACAAAGAAAGACCCCATGCGAGGAATATGATATGATGAAGAA 234  
|||

QY 204 TCTGGAAGAGGAATCAGATGAGGCACCTTAAATGACCATTCG 245  
|||

Db	233	CATGTATGAGGACGGTATGAGGAATGAGAGCAATTCG	192
RESULT 13			
LOCUS	BGL129051	724 bp mRNA linear	EST 31-JAN-2001
DEFINITION	EST474697 tomato shoot/meristem Lycopersicon esculentum cDNA clone		
ACCESSION	CF0F23M13	5' sequence, mRNA sequence.	
VERSION	BGL129051		
KEYWORDS	BGL129051.1	GI:12629239	
SOURCE	EST.		
ORGANISM	Lycopersicon esculentum (Solanum lycopersicum)		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.		
AUTHORS	1 (bases 1 to 724)		
TITLE	van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T., Hansen,C., Ronning,C. and Tanksley,S.		
JOURNAL	Generation of ESTs from tomato shoot/meristem tissue		
COMMENT	Unpublished (2001)		
CONTACT:	CUGI		
FEATURES	source		
	1..724		
	/organism="Lycopersicon esculentum"		
	/mol_type="mRNA"		
	/cultivar="TA496"		
	/db_xref="taxon:4081"		
	/clones="CF0F23M13"		
	/tissue_type="shoot/meristem"		
	/dev_stage="developing shoots from 4-6wks old plants"		
	/lab_host="SOLR"		
	/clone_lib="tomato shoot/meristem"		
	/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."		
ORIGIN			
	Query Match	5.5%; Score 38; DB 2; Length 724;	
	Best Local Similarity	60.8%; Pred. No. 11;	
	Matches	62; Conservative	0; Mismatches 40; Indels 0; Gaps 0;
QY	144	CACCTTGTGTCGACATCGAAACAGCCACTCGTCGAGGAAGCAGATGTCGACGAT	203
Db	536	CAAGCCTAGTGTGGACAAAGAAAGACCCATCGAGGAATATGATGATGAAGAA	595
QY	204	TCTGGAAGAGGAATCAGATGAGGCACCTTAAATGACCAATTCG	245
Db	596	CATGTATGAGGACGGTATGAGGAATGAGAGCAATTCG	637
RESULT 15			
LOCUS	BML13146	777 bp mRNA linear	EST 22-JAN-2002
DEFINITION	EST587473 tomato breaker fruit Lycopersicon esculentum cDNA clone		
ACCESSION	CL6G62M4	5' end, mRNA sequence.	
VERSION	BML13146		
KEYWORDS	BML13146.1	GI:18264776	
SOURCE	EST.		
ORGANISM	Lycopersicon esculentum (Solanum lycopersicum)		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.		
AUTHORS	1 (bases 1 to 777)		
	Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.B., Martin,G.B., Tanksley,S.D. and Giovannoni,J.		
TITLE	Generation of ESTs from tomato fruit tissue, breaker stage (2002)		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: CUGI		
	Clemson University Genomics Institute		
	Clemson University		
	100 Jordan Hall, Clemson, SC 29634, USA		
	Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a>		
	This clone is available through the Clemson University Genomics Institute		
	Seq primer: T3.		



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 23:54:43 ; Search time 433.327 Seconds  
(without alignments)  
10612.397 Million cell updates/sec

Title: US-10-734-373-59

Perfect score: 690

Sequence: 1 atgattcccaactgtgtc.....gaacaattgagccagaagtt 690

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: N\_Geneseq\_21.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001as.\*  
5: Geneseq2001bs.\*  
6: Geneseq2002as.\*  
7: Geneseq2002bs.\*  
8: Geneseq2003as.\*  
9: Geneseq2003bs.\*  
10: Geneseq2003cs.\*  
11: Geneseq2003ds.\*  
12: Geneseq2004as.\*  
13: Geneseq2004bs.\*  
14: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	690	100.0	888	4 AAD15679	Aad15679 Equine in
2	690	100.0	888	4 AAD15681	Aad15681 Equine in
3	690	100.0	891	4 AAD15678	Aad15678 Equine in
4	682	98.8	693	2 AAT37435	Aat37435 Non-struct
5	590.8	85.6	1146	3 AAA75003	Aaa75003 Nucleotid
6	578	83.8	824	14 ADY62118	Ady62118 Influenza
7	573.2	83.1	824	14 ADY62117	Ady62117 Influenza
8	570	82.6	890	12 ADO15247	Ado15247 Influenza
9	568.4	82.4	890	2 AAX82197	Aax82197 Influenza
10	568.4	82.1	890	6 ADW44527	Adw44527 Influenza
11	566.8	82.1	890	6 AAD37061	Aad37061 Influenza
12	557.2	80.8	890	2 AAQ23332	Aaq23332 RNA (+)
13	539.6	78.2	890	6 AB93942	Ab93942 Influenza
14	532.4	77.2	906	4 AAH77932	Aah77932 Nucleotid
15	291.4	42.2	468	4 AAD15680	Aad15680 Equine in
16	213.4	30.9	6010	2 AAT59676	Aat59676 Plasmid p
17	212.8	30.8	696	2 AAQ20237	Aaq20237 Encodes V
18	212.8	30.8	918	2 AAQ47361	Aaq47361 Sequence
19	212.8	30.8	918	2 AAQ70190	Aaq70190 Sequence

20	212.8	30.8	918	2 AAQ70208	Aaq70208 Sequence
21	212	30.7	453	2 AAT95097	Aat95097 Porcine s
22	212	30.7	453	6 AAD27035	Aad27035 Influenza
23	212	30.7	690	2 AAQ47362	Aaq47362 Sequence
24	212	30.7	690	2 AAQ70191	Aaq70191 Sequence
25	212	30.7	690	2 AAQ70209	Aaq70209 Sequence
26	212	30.7	924	2 AAQ04072	Aaq04072 Coding re
27	212	30.7	924	2 AAQ47364	Aaq47364 Sequence
28	212	30.7	924	2 AAQ70195	Aaq70195 Sequence
29	212	30.7	964	2 AAQ06580	Aaq06580 Plasmid s
30	212	30.7	1212	2 AAX87592	Aax87592 Haemagglu
31	211.6	30.7	681	2 AAQ47369	Aaq47369 Sequence
32	211.6	30.7	681	2 AAQ70201	Aaq70201 Sequence
33	211.6	30.7	717	2 AAQ47368	Aaq47368 Sequence
34	211.6	30.7	717	2 AAQ70200	Aaq70200 Sequence
35	211.6	30.7	729	2 AAQ04073	Aaq04073 Coding re
36	211.6	30.7	729	2 AAQ70197	Aaq70197 Sequence
37	211.6	30.7	912	2 AAQ70202	Aaq70202 Sequence
38	211.4	30.6	699	2 AAQ20236	Aaq20236 Encodes h
39	210.4	30.5	1014	2 AAQ38091	Aaq38091 NS1-19857
40	210.4	30.5	1017	2 AAQ38093	Aaq38093 NS1-783 f
41	210.4	30.5	1017	2 AAQ38092	Aaq38092 NS1-ACAI
42	210.4	30.5	1020	2 AAQ38090	Aaq38090 NS1-ZQ1 f
43	210	30.4	729	2 AAQ47365	Aaq47365 Sequence
44	210	30.4	912	2 AAQ47370	Aaq47370 Sequence
45	209.2	30.3	849	6 ABT08209	Abt08209 Breast ca

## ALIGNMENTS

RESULT 1  
AAD15679  
ID AAD15679 standard; DNA; 888 BP.

AC AAD15679;

DT 15-NOV-2001 (first entry)

DE Equine influenza virus H3N8 neiw3NS888 DNA.

KW Equine influenza virus; ei; cold adaptation; temperature sensitivity;

KW vaccine; neiw3NS888 DNA; ds.

OS Equine influenza virus H3N8.

PN WO200160849-A2.

XX 23-AUG-2001.

PF 16-FEB-2001; 2001WO-US005048.

PR 16-FEB-2000; 2000US-00506286.

XX (UYPI-) UNIV PITTSBURGH.

XX Dowling PW, Youngner JS;

XX WPI; 2001-522584/57.

XX Novel isolated equine influenza virus (wild-type and cold-adapted) proteins and viruses containing nucleic acid molecules encoding the proteins, which are useful for protecting animals from influenza virus infections.

XX Claim 2; Page 74; 172pp; English.

XX The patent discloses cold-adapted equine influenza viruses and reassortant influenza A viruses comprising at least one genome segment of such an equine influenza virus, wherein the equine influenza virus genome segment confers atleast one identifying phenotype of the cold-adapted equine influenza virus, such as cold adaptation, temperature sensitivity, dominant interference or attenuation. The viruses are useful for



Db 387 CAGCAATCATGATGAAGAACATCATATCTTAAAGCAAACTTTAGTGTGATTTTCGAAGG 446  
 Qy 421 CTGAGACACTAATATCTTCTAGAGCCTTCCACGAAGAAGAGAGAGAGTGGTGGCGAAAT 480  
 Db 447 CTGAGACACTAATATCTTCTAGAGCCTTCCACGAAGAAGAGAGAGTGGTGGCGAAAT 506  
 Qy 481 TCACCATTCCTTCTTCCAGGACATATTAATGAGATGTCACAAATGCAATTTGGGGTC 540  
 Db 507 TCACCATTCCTTCTTCCAGGACATATTAATGAGATGTCACAAATGCAATTTGGGGTC 566  
 Qy 541 CTCATCGAGAGACTTAAATGGAAATGATAATACGTTTGAATCTCTGAAATCTCTACAGAGA 600  
 Db 567 CTCATCGAGAGACTTAAATGGAAATGATAATACGTTTGAATCTCTGAAATCTCTACAGAGA 626  
 Qy 601 TTCGCTTGGAGAGAGAGTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
 Db 627 TTCGCTTGGAGAGAGAGTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 686  
 Qy 661 AAAATGGAG 690  
 Db 687 AAAATGGAG 716

## RESULT 3

AAD15678  
 ID AAD15678 standard; DNA; 891 BP.

AC AAD15678;

XX 15-NOV-2001 (first entry)

DT Equine influenza virus H3N8 neiwt1NS891 DNA.

XX Equine influenza virus; ei; cold adaptation; temperature sensitivity;  
 KW vaccine; neiwt1NS891 DNA; Peiwt1NS230 protein; ds.

XX Equine influenza virus H3N8.

XX Key Location/Qualifiers

FD 27, 719

FT /tag= a

FT /product= "Peiwt1NS230 protein"

FT 27, 716

FT /tag= b

FT /notes= "this region specifically claimed as SEQ ID NO: 34  
 in claim 2 of the specification"

XX WO200160849-A2.

XX 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US005048.

XX 16-FEB-2000; 2000US-00506286.

XX (UYP1-) UNIV PITTSBURGH.

XX Dowling PW, Youngner JS;

XX WPI; 2001-522584/57.

XX P-PSDB; AAE09027.

XX Novel isolated equine influenza virus (wild-type and cold-adapted)

XX PT proteins and viruses containing nucleic acid molecules encoding the

XX PT proteins, which are useful for protecting animals from influenza virus

XX PT infections.

XX Claim 2; Page 71-72; 172pp; English.

XX The patent discloses cold-adapted equine influenza viruses and

CC reasortant influenza A viruses comprising at least one genome segment of

CC segment confers at least one identifying phenotype of the cold-adapted  
 CC equine influenza virus, such as cold adaptation, temperature sensitivity,  
 CC dominant interference or attenuation. The viruses are useful for  
 CC protecting animals from diseases caused by influenza viruses. They are  
 CC also used as vaccines. The present sequence is an equine influenza (ei)  
 CC virus H3N8 neiwt1 (wild type) NS891 DNA encoding Peiwt1NS230 protein  
 XX

SQ Sequence 891 BP; 300 A; 174 C; 199 G; 218 T; 0 U; 0 Other;

Query Match 100.0%; Score 690; DB 4; Length 891;

Best Local Similarity 100.0%; Pred. No. 11e-212; Indels 0; Gaps 0;

Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGATTCCACACATGTCAGGCTTCAGGTAGACTGTTCTTTGGCATGTCGCAAA 60

Db 27 ATGGATTCCACACATGTCAGGCTTCAGGTAGACTGTTCTTTGGCATGTCGCAAA 86

Qy 61 CGATTTCGAGACCAAGAACTGGGTGATGCCCATTCCTTGCAGCGCTTCGCGAGACAG 120

Db 87 CGATTTCGAGACCAAGAACTGGGTGATGCCCATTCCTTGCAGCGCTTCGCGAGACAG 146

Qy 121 AAGTCCCTAAAAGGAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCTGTGCA 180

Db 147 AAGTCCCTAAAAGGAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCTGTGCA 206

Qy 181 GGAAAGCAGATAGTGGAGCAGAGATTCTTGAAGAGGAATCAGATGAGGCATTTAAATGACC 240

Db 207 GGAAAGCAGATAGTGGAGCAGAGATTCTTGAAGAGGAATCAGATGAGGCATTTAAATGACC 266

Qy 241 ATTGGCTCTGTTCTCTGCTTCAGCGTACTTAACTGACATGACTCTTGTATGAGATGCAAGA 300

Db 267 ATTGGCTCTGTTCTCTGCTTCAGCGTACTTAACTGACATGACTCTTGTATGAGATGCAAGA 326

Qy 301 GACTGGTTCATGCTCATGCCAAGCAGAGAAAGTAACAGGCTCCCTATGATATAGATGAC 360

Db 327 GACTGGTTCATGCTCATGCCAAGCAGAGAAAGTAACAGGCTCCCTATGATATAGATGAC 386

Qy 361 CAGCAATCATGATAGACATCATCTTAAAGCAAACTTTAGTGTGATTTTCGAAGG 420

Db 387 CAGCAATCATGATAGACATCATCTTAAAGCAAACTTTAGTGTGATTTTCGAAGG 446

Qy 421 CTGAGACACTAATATCTTCTAGAGCCTTCCACGAAGAAGAGAGAGTGGTGGCGAAAT 480

Db 447 CTGAGACACTAATATCTTCTAGAGCCTTCCACGAAGAAGAGAGAGTGGTGGCGAAAT 506

Qy 481 TCACCATTCCTTCTTCCAGGACATATTAATGAGATGTCACAAATGCAATTTGGGGTC 540

Db 507 TCACCATTCCTTCTTCCAGGACATATTAATGAGATGTCACAAATGCAATTTGGGGTC 566

Qy 541 CTCATCGAGAGACTTAAATGGAATGATAATACGTTTGAATCTCTGAAATCTCTACAGAGA 600

Db 567 CTCATCGAGAGACTTAAATGGAATGATAATACGTTTGAATCTCTGAAATCTCTACAGAGA 626

Qy 601 TTCGCTTGGAGAGAGTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660

Db 627 TTCGCTTGGAGAGAGTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 686

Qy 661 AAAATGGAG 690

Db 687 AAAATGGAG 716

## RESULT 4

NAT37435

ID AAT37435 standard; DNA; 693 BP.

XX AC AAT37435;

XX 16-OCT-2003 (revised)

DT 09-APR-1997 (first entry)

XX Non-structural protein NS1 of influenza A virus.

XX

KW Non-structural protein; NS1; influenza virus; respiratory tract;  
KW diagnosis; anti-NS1 antibody; primer; PCR; detection; amplify; ss.  
XX  
OS Influenza virus; A/equine 1/Suffolk 89.  
XX  
XX EP726316-A2.  
XX  
XX 14-AUG-1996.  
XX  
XX 31-JAN-1996; 96EP-00300681.  
XX  
XX 09-FEB-1995; 95GB-00002489.  
XX  
XX (ANIM-) ANIMAL HEALTH TRUST.  
XX  
XX Binns M, Birch-Machin I;  
XX  
XX WPI; 1996-364394/37.  
DR P-PSDB; AAW03522.  
XX  
XX Recombinant equine influenza virus NS1 protein - useful for diagnosis of  
PT equine influenza A.  
PT  
XX Claim 1; Fig 1A; 20pp; English.  
XX  
XX This sequence encodes non-structural protein NS1 of influenza virus  
CC A/equine 2/Suffolk 89. The NS1 protein is useful for diagnosis of equine  
CC influenza A infections by detection of anti-NS1 antibodies. The NS1  
CC coding sequence was isolated using the primer sequences given in AAT37436  
CC -40. (Updated on 16-OCT-2003 to standardise OS field)  
XX  
XX Sequence 693 BP; 215 A; 146 C; 166 G; 166 T; 0 U; 0 Other;  
SQ

Query Match 98.8%; Score 682; DB 2; Length 693;  
Best Local Similarity 99.3%; Pred. No. 3.8e-210;  
Matches 685; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
OY 1 ATGGATTCCAACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 60  
Db 1 ATGGATTCCAACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 60  
OY 61 CGATTTGACAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTCGCGAGACAG 120  
Db 61 CGATTTGACAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTCGCGAGACAG 120  
OY 121 AAGTCCCTAAAAGCAAGAGGTAGCTCTTGTCTGGACATCGAAACAGCCACTGTGCA 180  
Db 121 AAGTCCCTAAAAGCAAGAGGTAGCTCTTGTCTGGACATCGAAACAGCCACTGTGCA 180  
OY 181 GGAAGCGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATCAGGCACTTAAATGACC 240  
Db 181 GGAAGCGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACC 240  
OY 241 ATGGCTCTGTCTGCTTCAAGCTTAACTGACATGACTCTTGATGAGATGTCAAGA 300  
Db 241 ATGGCTCTGTCTGCTTCAAGCTTAACTGACATGACTCTTGATGAGATGTCAAGA 300  
OY 301 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATAGAATGGAC 360  
Db 301 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATAGAATGGAC 360  
OY 361 CAGGCAATCATGGATAGAACATCATCTACTTAAAGCAAACTTTAGTGTGATTTTCAAGG 420  
Db 361 CAGGCAATCATGGATAGAACATCATCTACTTAAAGCAAACTTTAGTGTGATTTTCAAGG 420  
OY 421 CTGGAGACACTAATCTACTTAGAGCTTTTACCGAAGAGGAGCAGTCGTTGGCGAAATT 480  
Db 421 CTGGAGACACTAATCTACTTAGAGCTTTTACCGAAGAGGAGCAGTCGTTGGCGAAATT 480  
OY 481 TCACCATTCGCTTCTCTTCCAGGACATCTAATGAGGATGTCAAAATGCAATTGGGGTC 540  
Db 481 TCACCATTCGCTTCTCTTCCAGGACATCTAATGAGGATGTCAAAATGCAATTGGGGTC 540

OY 541 CTCATCGGAGCCTTAATGAATGATAATAACGGTTTAGAATCTCTGAAACTCTACAGAGA 600  
Db 541 CTCATCGGAGCCTTAATGAATGATAATAACGGTTTAGAATCTCTGAAACTCTACAGAGA 600  
OY 601 TTGCTTTGGAGAGCAGTCATGAGAATGGGAGACCTTCATTCCCTCCAAAGCAGAAACGA 660  
Db 601 TTGCTTTGGAGAGCAGTCATGAGAATGGGAGACCTTCATTCCCTCCAAAGCAGAAACGA 660  
OY 661 AAAATGGAGNAGCAATTTGAGCAGAGTT 690  
Db 661 AAAATGGAGNAGCAATTTGAGCAGAGTT 690

## RESULT 5

AAAY5003/c

ID AAAY5003 standard; DNA; 1146 BP.

XX

AC AAAY5003;

XX

DT 02-JAN-2001 (first entry)

DE

XX Nucleotide sequence of an Influenza virus polynucleotide.

XX

KW Recombinant virus; vaccine; infection; hepatitis C virus vaccine;  
KW human immunodeficiency virus vaccine; HIV vaccine; tumour vaccine; ss.

XX

OS Influenza virus.

XX

PN EP1035209-A1.

XX

PD 13-SEP-2000.

XX

XX 06-MAR-1999; 99EP-00104519.

XX

PR 06-MAR-1999; 99EP-00104519.

XX

PA (ARTE-) ARTEMIS PHARM GMBH.

XX

PI Hobom G, Flick R, Menke A, Azzey M;

XX

DR WPI; 2000-559876/52.

XX

XX Recombinant influenza virus useful for gene therapy and as a vaccine  
PT against influenza and other infections, comprises viral RNA molecule  
PT exchanged for a viral RNA encoding foreign gene.

XX

PS Disclosure; Page 17-18; 49pp; English.

XX

CC The specification describes a recombinant influenza virus, which is  
CC genetically stable in the absence of helper virus. The influenza virus  
CC has at least one of the regular viral RNA segments exchanged for a viral  
CC RNA encoding a foreign gene. The virus also has at least one of the  
CC regular viral RNA segments in an ambisense RNA molecule containing one of  
CC the standard viral genes in sense orientation and a foreign, recombinant  
CC gene in anti-sense orientation, or vice versa. The recombinant viruses  
CC are useful for preparing vaccines in the form of inactivated preparations  
CC or live recombinant viruses which are protective against influenza and  
CC against other infections. The viruses are also useful in somatic gene  
CC therapy, for transfer and expression of foreign genes into cells infected  
CC by such viruses. They are also useful for design and production of  
CC hepatitis C virus, human immunodeficiency virus (HIV) and tumour  
CC vaccines. The present sequence represents an Influenza virus sequence  
CC which is used to produce viruses of the invention

XX

SQ Sequence 1146 BP; 271 A; 287 C; 233 G; 355 T; 0 U; 0 Other;

XX

Query Match 85.6%; Score 590.8; DB 3; Length 1146;

XX

Best Local Similarity 91.0%; Pred. No. 1.9e-180;

XX

Matches 628; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

XX

OY 1 ATGATTTCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 60

Db 1024 ATGATTTCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 965



Qy	61	CGATTG	CAGACCA	GAAGACT	GGTGAT	GCCCAAT	TCCTTG	ACCGGCT	TCGCGG	AGAC	CAG	120		
Db	964	CGATTG	CAGACCA	GAAGAA	GGTGAT	GCCCAAT	TCCTTG	ACCGGCT	TCGCGG	AGAT	CA	905		
Qy	121	AGTCCCT	TAAGA	AGAGG	ATGAC	CTCTTG	GTG	AGCAT	CGCAAA	CAGCC	ACT	TCGTGCA	180	
Db	904	AGTCCCT	TAGGGA	AGAGG	CAGCACT	CTTG	GTGTG	AGCAT	CGCACAC	AGCT	ACT	TCGTGTT	845	
Qy	181	GGAAAG	CAAGAT	GTGGAG	CAGCAAT	CTGGA	AGAGAA	TGAT	CAGAT	GAGCACT	TTAA	AAATCAAC	240	
Db	844	GGAAAG	CAAGAT	GTGGAG	CGGAAT	CTCGG	AGGACGA	ATCCG	TAGG	GACACT	TTAA	AAATGACC	785	
Qy	241	ATTGCCT	CTGTT	CTCTCT	TCACGCT	ACTT	AACTG	ATG	ATG	ATG	ATG	ATG	300	
Db	784	ATTGCCT	CTG	TACCTG	CTACAGCT	TACT	AACTG	ATG	ATG	ATG	ATG	ATG	725	
Qy	301	GACTGGT	TATG	CTCATG	CCCAAG	CAGAAAT	GAA	CAGCGCT	CCCTAT	GAT	TATG	ATG	360	
Db	724	GACTGGT	TATG	CTCATG	CCCAAA	CAGAAAT	GCGAGCGCT	CCCTTTG	GCAT	CAGA	ATG	GCAC	665	
Qy	361	CAGGCAAT	CATG	ATG	ATGAA	CAATCAT	ATAT	CTTAA	GCGAA	CAACTT	TATG	TGAT	420	
Db	664	CAGGCGAT	CATG	GGGAAG	CAATCAT	ATAT	CTG	AAAGCA	CAACTT	TCAT	TG	TGAT	605	
Qy	421	CTGGAG	ACAT	TATCTACT	GTAG	AGCCTT	CA	CCG	AGAGG	CGACG	TGTTG	CGCAAT	480	
Db	604	CTG	AACTCT	CATCTAT	TAA	GGGCTTT	AA	CCG	AT	GAGG	AGCAAT	TGT	CGGCAAT	545
Qy	481	TCACCAT	TGCTT	CTCTCC	AGGCA	CATACT	AT	ATG	AGGAT	GTCA	AAATG	CAAT	TGGGGTC	540
Db	544	TCACT	TTCCTCTCT	TC	CGAGCA	CACTACT	GT	ATG	AGGAT	GTCA	AAATG	CAAT	TGGGGTC	485
Qy	541	CTCAT	CGGAG	ACTTAA	TG	AGATG	ATA	TAT	ACGGT	TAG	ATCT	TG	AAATCT	600
Db	484	CTCAT	CGGAG	ACTTAA	TG	AGATG	ATA	TAT	ACAGAT	TTC	GT	CA	ATAT	425
Qy	601	TTGCT	TCG	AGAA	CGAGT	CAT	GAGA	ATGG	GAGAC	CTT	CA	TTCCT	CTCA	660
Db	424	TTGCT	TCG	AGAG	CGAGT	TAAT	GAGA	ATGGGG	GACCT	CC	AT	TCCCT	CTCA	365
Qy	661	AAAA	TGG	AGAA	CAAA	T	TGAG	CCAG	AA	AT				690
Db	364	AAAA	TGG	CGAA	CAAA	T	TGAGT	CA	AA	AT				335

RESULT 6	
ADY62118	ADY62118
ID	ADY62118 standard; DNA; 824 BP.
XX	
XX	ADY62118;
AC	
AC	
XX	
XX	19-MAY-2005 (first entry)
DT	
DT	
XX	Influenza A virus strain A/England/1/53v-a mutant NS1 gene for vaccine.
DE	
XX	
XX	protein engineering; immune stimulation; immunostimulant; vaccine;
KW	influenza virus infection; mutant; gene; ds.
KW	
XX	
XX	
OS	Influenza A virus; strain A/England/1/53v-a.

XX US2005054846-A1.  
PN XX  
XX  
PD 10-MAR-2005.  
XX  
XX  
PF 04-SEP-2003; 2003US-00654737.  
XX  
XX  
PR 04-SEP-2003; 2003US-00654737.

XX	(WEBS/) WEBSTER R G.
PA	(WEBB/) WEBBY R J.
PA	(OZAK/) OZAKI H.
XX	
PI	Webster RG, Webby RJ, Ozaki H;
PT	WPI; 2005-213104/22.
DR	P-FSDB; ADY62121.
XX	
PT	Producing a reassortant influenza virus that gives a high titer in Vero
PT	cells (certified for use in vaccine-production), comprises replacing the
PT	NS gene of the A/PuertoRico/3/24 master strain with the NS gene of the
PT	A/England/1/53 strain.
XX	
PS	Claim 8; SEQ ID NO 2; 16pp; English.
XX	
CC	The invention relates to a method of producing a high titer reassortant
CC	influenza virus by transfecting host cells with expression plasmids
CC	containing the PB2, PB1, PA, NP, and M genes from the A/PuertoRico/8/34
CC	influenza strain, the NS gene from the A/England/1/53 influenza strain,
CC	and the HA and NA genes from an influenza virus of interest other than
CC	A/England/1/53, to obtain a high titer reassortant influenza virus. The
CC	method is useful for producing a high titer reassortant influenza virus.
CC	The high titer reassortant influenza viruses are useful for producing
CC	vaccine compositions. The vaccines are useful for treating or preventing
CC	influenza viral infections. Genetic engineering techniques allow the
CC	rapid production of custom made attenuated virus vaccines, but vaccine
CC	use is limited by the need to use vaccine approved cell lines. The master
CC	strain A/PuertoRico/8/34 which is the most widely used in producing
CC	recombinant viruses for vaccine use produces a human titer in MDCK cells,
CC	which are not certified for use in production of human vaccines, but not
CC	in vero cells, which are certified for this use. The applicants have
CC	discovered that replacing the NS gene of the A/PuertoRico/3/24 master
CC	strain with the NS gene of the A/England/1/53 strain gives reassortant
CC	virus that produces a high titer in Vero cells. This sequence corresponds
CC	to the coding sequence for the NS1 protein from the A/England/1/53v-a
CC	influenza strain. This strain encodes the protein with the amino acid
CC	changes Q21R/T58I/V60A/NL27S/V174I/D189N/delta231-238.
XX	
SQ	Sequence 824 BP; 263 A; 167 C; 203 G; 191 T; 0 U; 0 Other;
Query Match      83.8%; Score 578; DB 14; Length 824;	
Best Local Similarity    89.9%; Pred. No. 2.3e-176;	
Matches 620; Conservative    0; Mismatches 70; Indels 0; Gaps 0;	
QY	1 ATGGATTCCAACACTGTGTCGAAGCTTTTCAGGTAGACTGTTTTCTTTTGGCATGTCGCGAAA 60
Db	6 ATGGATCCCAACACTGTGTCGAAGCTTTTCAGGTAGATTGCTTTCTTTGGCATGTCGCGAAA 65
QY	61 CGATTTSCAGACCMAAGACTGGGTGATGCCCATCTCTTGACCGGTCTGGCGAGACGACG 120
Db	66 CGAGTTGCAGACCCAGACTAGTGTATGCCCATCTCTTGTATCGGTCTGCGAGATCAG 125
QY	121 TAGTCCCTTAAGAGAGAGGTAGCACTCTTGCTGTGAGCATCGAAAGCCACTCTGTGCA 180
Db	126 AAGTCCCTTAGAGAGAGAGGCGACACTCTCGGGCTGTACATCGAACAGCATCCGTGCT 185
QY	181 GGAAAGCAGATAGTGGACAGATNTCTGGAAGAGGAGATCAGATAGGCGACTTAAATGACC 240
Db	186 GGAAAGCAAATATGTGAGCGGATTCGAAAGGAAGAATCCGATGAGGCGACTTAAATGACC 245
QY	241 ATTGCTCTCTTCTCTGTTCAAGCTACTTAACTGACATGACTCTTGATGAGATGTCAAGA 300
Db	246 ATFGGCTCTTCGACCTGCTTTCGGCTACTTAACTGACATGATAATTAGAGAAATGTCGAAG 305
QY	301 GACTGGTTCATGCTCATCCCCAGCAGAAAGTAAACAGGCTCCCTATGTATGAAGAAATGGAC 360
Db	306 GACTGGTTCATGCTCATCCCCAGCAGAAAGTGGCAGGCGCCCTCTTTGTATCAGAAATGGAC 365
QY	361 CAGGCAATCATGGATAAGAAACATCATCACTTAAAGCAAACCTTATGTGTGATTTTTCGAAGG 420
Db	366 CAGGCGATCATGGATAAGACATCATCACTTGAAGCGAACTTCAGTGTGATTTTGTGACGCG 425

QY 421 CTGGAGCACTAATACTACTAGAGCTTACCGAAGAGGAGCACTGTTGGCGAAATT 480  
 DB |||||||CTAATACTACTAGAGCTTACCGAAGAGGAGCACTGTTGGCGAAATT 485  
 QY 481 TCACCAATGGCTTCTCTCCAGACATCTAATGAGGATGTCAAAATGCAATTGGGGTC 540  
 DB |||||||CTAATACTACTAGAGCTTACCGAAGAGGAGCACTGTTGGCGAAATT 485  
 QY 541 CTCATCGGAGCACTAATGCAATGATATACGTTAGATCTCTGAACCTACAGAGA 600  
 DB |||||||CTAATACTACTAGAGCTTACCGAAGAGGAGCACTGTTGGCGAAATT 485  
 QY 546 CTCATCGGAGCACTAATGCAATGATATACGTTAGATCTCTGAACCTACAGAGA 605  
 DB |||||||CTAATACTACTAGAGCTTACCGAAGAGGAGCACTGTTGGCGAAATT 485  
 QY 601 TTCGCTTGGAGAGCAGTCATGAGAAATGGGAGACCTTCCTCCAAAGCAGAAACGA 660  
 DB |||||||CTAATACTACTAGAGCTTACCGAAGAGGAGCACTGTTGGCGAAATT 485  
 QY 661 AAAATCGGAGAACAAATGAGCCGAGAAATT 690  
 DB |||||||CTAATACTACTAGAGCTTACCGAAGAGGAGCACTGTTGGCGAAATT 485  
 QY 666 AAAATCGGAGAACAAATGAGCCGAGAAATT 695

## RESULT 7

ADY62117  
 ID ADY62117 standard; DNA; 824 BP.

AC ADY62117;

DT 19-MAY-2005 (first entry)

DE Influenza A virus strain A/England/1/53 wild type NS1 gene for vaccine.

XX protein engineering; immune stimulation; immunostimulant; vaccine;

KW influenza virus infection; gene; ds.

XX Influenza A virus; strain A/England/1/53.

XX Key Location/Qualifiers

FT 6..719

FT /\*tag= a

FT /product= "influenza A virus NS1 protein"

FT /note= "no stop codon given"

XX US2005054846-A1.

XX 10-MAR-2005.

XX 04-SEP-2003; 2003US-00654737.

XX 04-SEP-2003; 2003US-00654737.

XX (WEBS/) WEBSTER R G.

XX (WEBB/) WEBBY R J.

XX (OZAK/) OZAKI H.

XX Webster RG, Webby RJ, Ozaki H;

XX WPI; 2005-213104/22.

XX P-PSDB; ADY62119.

XX Producing a reassortant influenza virus that gives a high titer in Vero cells (certified for use in vaccine-production), comprises replacing the NS gene of the A/PuertoRico/3/24 master strain with the NS gene of the A/England/1/53 strain.

XX Claim 7; SEQ ID NO 1; 16pp; English.

XX The invention relates to a method of producing a high titer reassortant influenza virus by transfecting host cells with expression plasmids containing the PB2, PB1, PA, NP, and M genes from the A/PuertoRico/8/34 influenza strain, the NS gene from the A/England/1/53 influenza strain, and the HA and NA genes from an influenza virus of interest other than A/England/1/53, to obtain a high titer reassortant influenza virus. The

CC method is useful for producing a high titer reassortant influenza virus.  
 CC The high titer reassortant influenza viruses are useful for producing  
 CC vaccine compositions. The vaccines are useful for treating or preventing  
 CC influenza viral infections. Genetic engineering techniques allow the  
 CC rapid production of custom made attenuated virus vaccines, but vaccine  
 CC use is limited by the need to use vaccine approved cell lines. The master  
 CC strain A/PuertoRico/8/34 which is the most widely used in producing  
 CC recombinant viruses for vaccine use produces a high titer in MDCK cells,  
 CC which are not certified for use in production of human vaccines, but not  
 CC in Vero cells, which are certified for this use. The applicants have  
 CC discovered that replacing the NS gene of the A/PuertoRico/3/24 master  
 CC strain with the NS gene of the A/England/1/53 strain gives reassortant  
 CC virus that produces a high titer in Vero cells. This sequence corresponds  
 CC to the coding sequence for the NS1 protein from the A/England/1/53  
 CC influenza strain.

XX SQ Sequence 824 BP; 267 A; 167 C; 201 G; 189 T; 0 U; 0 Other;

Query Match 83.1%; Score 573.2; DB 14; Length 824;

Best Local Similarity 89.4%; Pred. No. 8.2e-175;

Matches 617; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1 ATGGATTCGAACACTGCTGCTCAAGCTTTCAGTAGTACTGTTTCTTGGCATGTCGCCAAA 60

DB 6 ATGGATTCGAACACTGCTGCTCAAGCTTTCAGTAGTACTGTTTCTTGGCATGTCGCCAAA 65

QY 61 CGATTTCAGACCAAGAACTGGGTGATGCCCACTTCTTGACCGGCTTCGCCGAGACAG 120

DB 66 CAAATTGCAGACCAAGAACTGGGTGATGCCCACTTCTTGACCGGCTTCGCCGAGACAG 125

QY 121 AAGTCCCTAAAGGAAGAGGTAGCACTTTGGTTCGACATCGAAGCAAGCACTCTCGTCA 180

DB 126 AAGTCCCTAAAGGAAGAGGTAGCACTTTGGTTCGACATCGAAGCAAGCACTCTCGTCA 185

QY 181 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGAAATCAGATGAGGCACTTAAATGACC 240

DB 186 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGAAATCAGATGAGGCACTTAAATGACC 245

QY 241 ATTGCCTCTGTTCTCTGCTTTCAGCTTAACTGAATCACTCTTGTGATGATGTCAAGA 300

DB 246 ATGGCTCCCGCACTCTCTGCGATACCTAACTGATGATGAGGAAATGTCAAGG 305

QY 301 GACTGGTTTCATGCTCATGCCCAAGCAGAAAGTAACAGGCTCCCTATGATATAAGAAATGAC 360

DB 306 GACTGGTTTCATGCTCATGCCCAAGCAGAAAGTAACAGGCTCCCTATGATATAAGAAATGAC 365

QY 361 CAGCAATCATGGATTAAGAAACATCATATTTAAAGCAAACTTTAGTGTGATTTTCAAGG 420

DB 366 CAGCGATCATGGATTAAGAAACATCATATTTAAAGCAAACTTTAGTGTGATTTTCAAGG 425

QY 421 CTGGAGACACTAATACTACTTAGAGCCCTTACCGAAGAGGAGCAGTCTGTTGGCGAAATT 480

DB 426 CTGGAGACACTAATACTACTTAGAGCCCTTACCGAAGAGGAGCAGTCTGTTGGCGAAATT 485

QY 481 TCACCAATGGCTTCTCTTCCAGGACATATAATGAGGATGTCAAAAATGCAATTTGGGGTC 540

DB 486 TCACCAATGGCTTCTCTTCCAGGACATATAATGAGGATGTCAAAAATGCAATTTGGGGTC 545

QY 541 CTCATCGGAGCACTTAAATGGAATGATATACGGTTAGAAATCTCTGAAACTCTACAGAGA 600

DB 546 CTCATCGGAGCACTTAAATGGAATGATATACGGTTAGAAATCTCTGAAACTCTACAGAGA 605

QY 601 TTCGCTTGGAGAGCAGTCTAGAAATGAGGAGACCTTCATTCCTCCAAAGCAGAAACGA 660

DB 606 TTCGCTTGGAGAGCAGTCTAGAAATGAGGAGACCTTCATTCCTCCAAAGCAGAAACGA 665

QY 661 AAAATGGAGCAACAAATGAGCCGAGAAATT 690

DB 666 AAAATGGAGCAACAAATGAGCCGAGAAATT 695

RESULT 8  
 ADO15247

ID ADO15247 standard; DNA; 890 BP.  
 XX ADO15247;  
 AC  
 XX 12-AUG-2004 (first entry)  
 DT  
 XX Influenza virus non-structural protein ISDN 13426 DNA.  
 DE  
 XX vaccine; T-cell epitope; antibody; B-cell receptor; CD40; CD28;  
 KW immune response; immunisation; antibacterial; virucide; antiparasitic;  
 KW fungicide; antiaddictive; cytostatic; bacterial antigen; virus antigen;  
 KW parasite antigen; fungal antigen; influenza virus; gene; ds.  
 XX  
 OS Influenza virus.  
 XX  
 XX WO2004041866-A1.  
 PN  
 XX 21-MAY-2004.  
 PD  
 XX 03-NOV-2003; 2003WO-GB004738.  
 PF  
 XX 05-NOV-2002; 2002GB-00025736.  
 PR  
 XX (ADJU-) ADJUVANTIX LTD.  
 PA  
 XX Heath A;  
 PI  
 XX WPI; 2004-400648/37.  
 DR  
 XX Vaccine composition for immunizing humans or animals against T-cell  
 PT independent antigens, e.g. bacteria, viruses, parasites or fungi,  
 PT comprises antibodies against B-cell receptor CD40 or CD28.  
 PT  
 XX Disclosure; Fig 16; 51pp; English.  
 XX  
 XX The present invention describes a vaccine composition (I) comprising a  
 CC conjugate comprising a carrier group having a T-cell epitope and an  
 CC adjuvant, where the adjuvant is an antibody, or its binding part, which  
 CC binds the B-cell receptor CD40 or CD28 and a second conjugate comprising  
 CC a second carrier group comprising a T-cell epitope and an antigen to  
 CC which an immune response is desired. Also described: (1) methods of  
 CC immunising an animal to an antigen; (2) an antibody obtained by the above  
 CC method, which binds the antigen part of the second conjugate; (3) a  
 CC method for preparing a hybridoma cell-line producing monoclonal  
 CC antibodies described above; and (4) a hybridoma-cell line obtained by the  
 CC above method. (I) has antibacterial, virucide, antiparasitic, fungicide,  
 CC antiaddictive and cytostatic activities, and can be used in vaccines. The  
 CC composition (I) and methods are useful for immunising humans or animals  
 CC against T-cell independent antigens, such as bacteria, viruses, parasites  
 CC or fungi. The present sequence represents an influenza virus nucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 890 BP; 283 A; 180 C; 215 G; 212 T; 0 U; 0 Other;  
 Query Match 82.6%; Score 570; DB 12; Length 890;  
 Best Local Similarity 89.1%; Pred. No. 9.3e-174;  
 Matches 615; Conservative 0; Mismatches 75; Indels 0; Gaps 0;  
 QY 1 ATGGATTCACACACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCCGAAA 60  
 DB 27 ATGGATTCACACACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCCGAAA 86  
 QY 61 CGATTTTCGAGACCAAGAACTGGGTGATGCCCATTCCTTTGACCGGCTTCCCGAGACAG 120  
 DB 87 CGAGTTTCGAGACCAAGAACTAGGTGATGCCCATTCCTTTGATCGGCTTCCCGAGATCAG 146  
 QY 121 AAGTCCCTAAAGAGAGAGTAGACACTTTGGTCTGACATCGAAACAGCCACTCTGTGCA 180  
 DB 147 AATCCCTTAAGAGAGAGGCGAGTACTCTCGTCTGACATCAAGACGACCACTGTCT 206  
 QY 181 GGAAGCAGATAGTGGAGCAGATTTCTGAGAGAGATCAGATGAGGACCTTAAATGACC 240  
 DB 207 GGAAGCAGATAGTGGAGCAGATTTCTGAGAGAGATCCGATGAGGACCTTAAATGACC 266

QY 241 ATTGCCTCTGTTCCTGCTTCAACGCTACTTAACTGACATGACTCTTGATGAGATGTCAAGA 300  
 DB 267 ATGGCCTCTGTACCTGCGTGCCTTAACTGACATGACTCTTGAGGAAATGTCAAGG 326  
 QY 301 GACTGCTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTCTGTATGATAAGATGAC 360  
 DB 327 GACTGCTCATGCTCATACCAGCAGAAAGTGGCAGGCCCTCTTTGTATCAGATGAC 386  
 QY 361 CAGGCAATCATGATAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTCCAAAGG 420  
 DB 387 CAGGCGATCATGATAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTCCCGG 446  
 QY 421 CTGGAGACACTAATACTACTTAGAGCCTTCAACGAGGAGGAGCAGTCTGTCGCGAATT 480  
 DB 447 CTGGAGACTCTAATATTGCTTAGGGCTTTCACCGAGGAGGAGCAATTTTGGCGAATT 506  
 QY 481 TCACCATTTGCTCTCTCTCCAGGACATCTAATGAGATGTCAAAATCAATTCGGGTC 540  
 DB 507 TCACCATTTGCTCTCTCTCCAGGACATCTCTGAGATGTCAAAATCAATTCGGGTC 566  
 QY 541 CTCATCGGAGGACTTAAATGGAATGATATACGGTTAGAAATCTCTGAAACTCTACAGAGA 600  
 DB 567 CTCATCGGAGGACTTGAATGGAATGATATACAGAGTTCGAGTCTCTGAAACTCTACAGAGA 626  
 QY 601 TTGCTTTGGAGAGCAGTCAATGAGAAATGGAGAGACTTTCATTCCTCCAAAGCAGAAACGA 660  
 DB 627 TTGCTTTGGAGAGCAGTCAATGAGAAATGGAGAGACTTTCATTCCTCCAAAGCAGAAACGA 686  
 QY 661 AAAATGGAGAGAACTTGAATGGAATGAGAAATGGAGAGACTTTCATTCCTCCAAAGCAGAAACGA 690  
 DB 687 GAAATGGGCGGAACTTGAATGGAATGAGAAATGGAGAGACTTTCATTCCTCCAAAGCAGAAACGA 716  
 RESULT 9  
 AAX82197  
 ID AAX82197 standard; DNA; 890 BP.  
 XX  
 AC AAX82197;  
 XX 18-AUG-1999 (first entry)  
 DT  
 DE Influenza virus NS protein gene sequence.  
 XX  
 KW Cold-adapted influenza virus; passage culture; PB2 protein; PB1 protein;  
 KW PA protein; NP protein; M protein; NS protein; temperature sensitivity;  
 KW vaccine; flu; influenza; ss.  
 XX  
 OS Influenza virus.  
 XX  
 PN WO9928445-A1.  
 PD  
 PD 10-JUN-1999.  
 XX  
 PF 30-NOV-1998; 98WO-KR000384.  
 XX  
 PR 29-NOV-1997; 97KR-00064854.  
 XX  
 XX (CHEI-) CHEIL JEDANG CORP.  
 PA  
 PI Seong BL, Lee KH, Youn JW, Kim SJ, Cheoun KH, Kim J, Kim HG;  
 XX WPI; 1999-385377/32.  
 DR  
 XX Cold-adapted influenza viruses useful for the production of protective  
 PT vaccines against flu.  
 PT  
 PS Claim 4; Page 58; 62pp; English.  
 XX  
 CC The invention relates to cold-adapted influenza viruses prepared by  
 CC passage culture of A/X-31, B/Yamagata/16/88 or B/Lee/40 viruses at low  
 CC temperatures. A cDNA gene of cold-adapted influenza virus H5N1 can  
 CC be selected from a group consisting of PB2 protein gene, PB1 protein



QY 301 GACTGGTTCATGCTCATGCCCAGCAGAAAGTAACAGGCTCCCTATGTATGAAGAATGGAC 360  
 Db 327 GACTGGTTCATGCTCATACCCCAAGCAGAAAGTGGCAGGCCCTCTTTGTATCAGAATGGAC 386  
 QY 361 CAGCAATCATGATGAAGAATCATATCTTAAAGCAAACTTTAGTGTGATTTTCGAAGG 420  
 Db 387 CAGCGATCATGATGAAGAATCATATCTGAAAGCGCAACTTCAGTGTGATTTTCACCGG 446  
 QY 421 CTGAGACACTAATATCTTCTAGAGCCCTTCACCGAAGAGGAGCAGTCGTTGCGCAAAAT 480  
 Db 447 CTGAGACACTAATATCTTCTAGAGCCCTTCACCGAAGAGGAGCAGTCGTTGCGCAAAAT 506  
 QY 481 TCACCATTCCTCTCTCCAGGACATATCTAATGAGGATGTCAAAAATGCAATTTGGGTC 540  
 Db 507 TCACCATTCCTCTCTCCAGGACATATCTGCTGAGGATGTCAAAAATGCAATTTGGGTC 566  
 QY 541 CTATCGAGGACTTAAATGGAATGATAATACGTTTAGAATCTCTGAACTCTACAGAGA 600  
 Db 567 CTCATCGAGGACTTGAATGGAATGATAACACAGTTCGAGTCTCTGAACTCTACAGAGA 626  
 QY 601 TTGCTTTGGAGAGCAGTCATGAGATGGGAGACCTTCATTCCTCCCAAGCAGAAAGA 660  
 Db 627 TTGCTTTGGAGAGCAGTCATGAGATGGGAGACCTTCATTCCTCCCAAGCAGAAAGA 686  
 QY 661 AAATGGAGAGCAATTTGAGCCGAGATT 690  
 Db 687 GAAATGGCGGAAACAAATTAGGTCAGAAATT 716

## RESULT 11

AAD37061  
 ID AAD37061 standard; cDNA; 890 BP.

XX AC AAD37061;

XX 21-AUG-2002 (first entry)

XX Influenza A virus/singapore/1/57/ca NS mutant cDNA.

XX Attenuated influenza vaccine; prophylactic; therapeutic; infection;  
 virulence; gene; NS1 protein; NS2 protein; mutant; ss.

XX Influenza A virus.

XX Synthetic.

XX Key Location/Qualifiers

XX CDS 27..864

XX /tag= b

XX /product= "NS2 mutant protein"

XX /transl\_except= (pos:48..525, aa:Asn-Leu)

XX CDS 27..740

XX /tag= a

XX /product= "NS1 mutant protein"

XX mutation replace(813, A)

XX /tag= c

XX WO200224876-A2.

XX 28-MAR-2002.

XX 25-SEP-2001; 2001WO-BF011087.

XX 25-SEP-2000; 2000EP-00120896.

XX (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.

XX Kateringer H, Egorov A, Ferko B, Romanova J, Kateringer D;

XX WPI; 2002-416282/44.

XX P-PSDB; AAE23116, AAE23117.

XX Manufacturing live vaccine, by infecting Vero cells with virus, combining  
 cells with serum-free cell culture medium, incubating cells in presence

PT of protease and nuclease, harvesting virus and preparing vaccine.  
 XX Example 4; Page 44; 90pp; English.  
 XX The present invention relates to a method for isolating viruses from  
 CC various sources and for producing live attenuated influenza vaccines in a  
 CC serum-free African green monkey kidney (Vero) cell culture under  
 CC conditions where alterations in the surface antigens of the virus due to  
 CC adaptive selection are minimised or prevented. The method is useful for  
 CC the manufacture of whole-virus vaccine, preferably attenuated live  
 CC vaccine. It is useful for prophylactic or therapeutic administration  
 CC against viral infection, preferably influenza virus infections. The  
 CC present sequence is influenza A virus/singapore/1/57/ca (cold adapted)  
 CC mutant cDNA encoding NS1 and NS2 protein. This sequence is used in the  
 CC exemplification of the invention

XX Sequence 890 BP; 294 A; 178 C; 207 G; 211 T; 0 U; 0 Other;

Query Match 82.18; Score 566.8; DB 6; Length 890;

Best Local Similarity 88.88; Pred. No. 1e-172;

Matches 613; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 1 ATGGATTCACACACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCCGAAA 60  
 Db 27 ATGGATTCACACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCCGAAA 86  
 QY 61 CGATTTCGAGACCAGAACTTGGGTGATGCCCTTCCTTCAACCGCTTCGCGAGACGAG 120  
 Db 87 CAAGTTGCAGACCAAGAACTAGGTGATGCCCTTCCTTCAACCGCTTCGCGAGACGAG 146  
 QY 121 AAGTCCCTAAAAGGAGAGTAGTACACTCTTGGTCTGGACATCGAAACAGCCACTCGTGA 180  
 Db 147 AAGTCCCTAAGGGAGAGGAGGAGCACTCTCGGTCTGAACATCGAAACAGCCACTCGTGT 206  
 QY 181 CGAAAGCAGATAGTGGAGCAGATTCTTGAAGAGGAATCCAGATGAGGACCTTAAATGACC 240  
 Db 207 CGAAAGCAGATAGTGGAGCAGATTCTTGAAGAGGAATCCAGATGAGGACCTTAAATGACC 266  
 QY 241 ATTGCTCTGTCTCTCTTCCAGCTTCTTCAAGCTTAACTGACATGACTCTTGTATGAGATGCAAGA 300  
 Db 267 ATGGCTCCGACCTCTCTTCCGATACCTTAATGACATGACTTATGAGGAAATGTCAGG 326  
 QY 301 GACTGTTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATAGATGGAC 360  
 Db 327 GACTGTTTCATGCTTAATGCCCAAGCAGAAAGTAAACAGGCTCTTGTATGAGATGGAC 386  
 QY 361 CAGCAATCATGATGAAGAATCATATCTTAAAGCAAACTTTAGTGTGATTTTCGAAGG 420  
 Db 387 CAGCGATCATGATGAAGAATCATATCTTAAAGCGCAATTCAGTGTGATTTTCACCGG 446  
 QY 421 CTGAGACACTAATATCTTCTAGAGCCCTTCACCGAAGAGGAGCAGTCGTTGCGCAAAAT 480  
 Db 447 CTAGAGACCTTAATATCTTCTAGAGCCCTTCACCGAAGAGGAGCAGTCGTTGCGCAAAAT 506  
 QY 481 TCACCATTCCTCTCTTCCAGGACATATCTAATGAGGATGTCAAAAATGCAATTTGGGTC 540  
 Db 507 TCACCATTCCTCTCTTCCAGGACATATCTAATGAGGATGTCAAAAATGCAATTTGGGTC 566  
 QY 541 CTCATCGGAGGACTTAAATGGAATGATATACGGTGTAGAACTCTCTGAACTCTACAGAGA 600  
 Db 567 CTCATCGGAGGACTTGAATGGAATGATATACAGTTCGAGTCTCTGAACTCTACAGAGA 626  
 QY 601 TTGCTTTGGAGAGCAGTCATGAGATGGGAGACCTTCAATTCCTCCAAAGCAGAAAGA 660  
 Db 627 TTGCTTTGGAGAGCAGTCATGAGATGGGAGACCTTCAATTCCTCCAAAGCAGAAAGA 686  
 QY 661 AAATGGAGAGCAATTTGAGCCGAGATT 690  
 Db 687 AAATGGCGGAAACAAATTAGGTCAGAAATT 716

RESULT 12  
 AAO22332



SQ Sequence 890 BP; 296 A; 176 C; 208 G; 210 T; 0 U; 0 Other;  
 Query Match 78.2%; Score 539.6; DB 6; Length 890;  
 Best Local Similarity 86.4%; Pred. No. 6.8e-164;  
 Matches 596; Conservative 0; Mismatches 94; Indels 0; Gaps 0;  
 QY 1 ATGGATTCCAAACACGTGTCTCAAGCTTTTCAGTAGAGCTTTTCTTTGSCATGTCGCGAAA 60  
 DB 27 ATGGATTCCAAACACGTGTCTCAAGCTTTTCAGTAGAGCTTTTCTTTGSCATGTCGCGAAA 86  
 QY 61 CGATTTCGAGACCAAGAACTCGGTGATGCCCACTTCCCTGACCGCTTCGCGAGCAG 120  
 DB 87 CAAGTTGTAGACCAAGAACTAGGTGATGCCCACTTCCCTGATCGCTTCGCGAGATCAG 146  
 QY 121 AAGTCCCTAAAGGAGAGGTAGCACTCTGTGCTGGCATCGAAAGCAGCACTCTGTGCA 180  
 DB 147 AAGTCCCTAAGGAGAGGAGCGACCTCTCGGTCTAAATCGAAGCGCCACCAATGTT 206  
 QY 181 GGAACGATAGTCGAGCAGATTCTGGAAGAGCAATCGATGAGGCACTTAAATGACC 240  
 DB 207 GGAAGCAGATAGTAGAAGATTCTGAAGAGCAATCTGATGAGGCACTTAAATGACC 266  
 QY 241 ATTGCTCTGTTCTGCTTCAGCTACTTAACTGACATGACTCTTGTGATGAGATGTCAGAA 300  
 DB 267 ATGGCTCTCACACCTGCTTCGCGATACATCACTGACATGACTATTGAGGAATTGTCAGG 326  
 QY 301 GACTGGTTCATCTCATGCCCAAGCAGAAAGTAACAGGCTCCCTATGTATATAAGAAATGGAC 360  
 DB 327 GACTGGTTCATCTAATGCCCAAGCAGAAAGTGAAGGACCTCTTTGCATCAGAAATAGAC 386  
 QY 361 CAGGCAATCATGGATAAGAACATCATACTTAAAGCAAACTTAGTGTGATTTTCGAAGG 420  
 DB 387 CAAGCAATCATGGATAAGAACATCATCTTGAAGCGAAATTCAGTGTGATTTTCAGCGG 446  
 QY 421 CTGGAGACCTAATACTACTTACTTAGAGCTTCCACGAGAGGAGGAGCTGTTGCGCAAT 480  
 DB 447 CTAGAGACCTAATACTAATAAGGCTTTCCACGAGAGGAGGCAATTTGTTGCGCAATC 506  
 QY 481 TCACCATTCGCTCTCTTCCAGGACATCTAATGAGGATGTCAAATGCAATTTGGGGTC 540  
 DB 507 TCACCATTCGCTCTCTTCCAGGACATCTAATGAGGATGTCAAATGCAATTTGGGGTC 566  
 QY 541 CTGATCGGAGGACTTAAATGGAATGATATACGCTTGAATCTCTGAACTCTACAGAGA 600  
 DB 567 CTATCGAGGACTTGAATGGAATGATACACAGTTCGAGTCTCTAAACTCTACAGAGA 626  
 QY 601 TTGCTTGGAGAGCAGTCATGAGATGGGAGACCTTCATTCCTCCAAAGCAGAAACGA 660  
 DB 627 TTGCTTGGGAGAGCAGTAATGAGATGGGAGACCTTCCACTTACTCCAAACAGAAACGG 686  
 QY 661 AAAATGGAGAGCAATTTGACCCAGAGTT 690  
 DB 687 AAAATGGGAGAACAGCTAGTCAAAAGTT 716

## RESULT 14

AAH77932

ID AAH77932 standard; DNA; 906 BP.

XX

AC AAH77932;

XX

DT 13-NOV-2001 (first entry)

XX

DE Nucleotide sequence of PR8NS38.

XX

KW Nonstructural gene; NS gene; influenza A virus; NSI gene; vaccine;

XX viral infection; influenza infection; HIV-1 infection; ss.

XX

OS Unidentified.

XX

PN W0200164860-A2.

XX

FD 07-SEP-2001.

XX 02-MAR-2001; 2001WO-EP002392.  
 PF 02-MAR-2000; 2000EP-00104338.  
 PR (POLY-) POLYMER SCI IMMUNOBIOLOGISCHE FORSCHUNG.  
 XX Ferko B, Egorov A, Voglauer R;  
 XX WPI; 2001-514840/56.  
 XX Recombinant NS gene of an influenza A virus comprising a functional RNA  
 binding domain and a gene sequence modification after nucleotide position  
 400 of the NSI gene segment, useful for producing a live attenuated  
 influenza virus vaccine.  
 XX Example 6; Page 21; 40pp; English.  
 XX The specification describes a recombinant nonstructural (NS) gene of an  
 influenza A virus. The gene comprises a functional RNA binding domain and  
 a gene sequence modification after nucleotide position 400 of the NSI  
 gene segment, counted on the basis of influenza A/PR/8/34 virus, where  
 the modification bars transcription of the remaining portion of the NSI  
 gene segment. The recombinant NS gene is used to produce a vaccine, which  
 is useful for prophylactic or therapeutic application against a viral  
 infection, preferably against influenza or HIV-1 infection. Influenza  
 virus transfectants that contain the modified NS gene may have an  
 interferon (IFN) inducing phenotype, but may or may not be sensitive  
 towards IFN. The present sequence was used to construct vectors for  
 production of modified NS genes of the invention  
 XX Sequence 906 BP; 288 A; 183 C; 221 G; 214 T; 0 U; 0 Other;  
 SQ  
 Query Match 77.2%; Score 532.4; DB 4; Length 906;  
 Best Local Similarity 87.0%; Pred. No. 1.5e-161;  
 Matches 614; Conservative 0; Mismatches 76; Indels 16; Gaps 2;  
 QY 1 ATGGATTCCAAACACGTGTCTCAAGCTTTTCAGTAGAGCTTTTCTTTGSCATGTCGCGAAA 60  
 DB 27 ATGGATTCCAAACACGTGTCTCAAGCTTTTCAGTAGAGCTTTTCTTTGSCATGTCGCGAAA 86  
 QY 61 CGATTTCGAGACCAAGAACTCGGTGATGCCCACTTCCCTGACCGCTTCGCGAGCAG 115  
 DB 87 CAAGTTGTAGACCAAGAACTAGGTGATGCCCACTTCCCTGATCGCTTCGCGAGATCAG 146  
 QY 116 -----ACGAAAGTCCCTTAAAGAGAGAGGTAGCACTTTGGTCTGGACATCGAA 165  
 DB 147 AACTAGCTGAATCAGAAATCCCTAAGAGAGAGGAGGAGCACCCTCGGTCTGGACATCGAG 206  
 QY 166 ACAGCCACTCTGCGAGAAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATCAG 225  
 DB 207 ACAGCCACACGTGCTGGAAGAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATCAG 266  
 QY 226 GCACCTTAAATGACCATTTGCTCTGTTCTCTTCAAGCTACTTAACTGACATGACTCTT 285  
 DB 267 GCACCTTAAATGACCATTTGCTCTGTTCTCTTCAAGCTACTTAACTGACATGACTCTT 326  
 QY 286 GATGAGATGTCAGAGACGCTGTTTCATGCTGATGCCCAAGCAGAGAAAGTAACAGGCTCCCTA 345  
 DB 327 GAGGAAATGTCAGGAGACTGGTCCATGCTCATCCCAAGCAGAGAAAGTGGCAGGCTCTT 386  
 QY 346 TGTATAAGAAATGGACCAAGCAATCATGGA-TAAGAAATCATACTTAAAGCAAACTTTAG 404  
 DB 387 TGTATCAGAAATGGACCAAGCAATCATGGA-TAAGAAATCATACTTAAAGCAAACTTTAG 446  
 QY 405 TGTGATTTTCCAAAGGCTGGAGACACTAATACTACTTAGAGCTTCCACCGRAGAGGAGC 464  
 DB 447 TGTGATTTTGAAGGCTGGAGACTTAATATTGCTTAAGGCTTTTCCCGAAGAGGAGC 506  
 QY 465 AGTCGTTGGGCAAAATTTCCACCATTCGCTTCTTCTCGAGGACATACTAATGAGAGTGTCAA 524  
 DB 507 AATTGTTGGGCAAAATTTCCACCATTCGCTTCTTCTCGAGGACATACTGCTGAGAGTGTCAA 566

```
QY 525 AATGCAATTGGGTCCTCATCGAGGACTTAATGGAATGATAATACGGTTAGAAATCTC 584
Db 567 AATGCAATTGGGTCCTCATCGGAGGACTTGAATGGAATGATAATACCAATTCGAGTCTC 626
QY 585 TGAATCTCTACAGAGATTCGTTGGAGAGCAGTCAATGAGATGGAGACCTTCATCCCC 644
Db 627 TGAATCTCTACAGAGATTCGTTGGAGAGCAGTCAATGAGATGGAGACCTTCACCTCAC 686
QY 645 TCCAAAGCAGAAACGAAATGAGAGAGAACAAATGAGCCAGAAAGTT 690
Db 687 TCCAAAGCAGAAACGAGAAATGCGCGGACAAATAGGTTCAGAAAGTT 732

RESULT 15
AADI5680
ID AADI5680 standard; DNA; 468 BP.
AC AADI5680;
XX
XX 15-NOV-2001 (first entry)
XX
XX Equine influenza virus H3N8 neiwt4NS468 DNA.
XX
XX Equine influenza virus; ei; cold adaptation; temperature sensitivity;
KW vaccine; neiwt4NS468 DNA; Peiwt4NS97 protein; ds.
XX
XX Equine influenza virus H3N8.
XX
XX
FH Key Location/Qualifiers
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FT /*tag= b
FT /note= "This region is specifically claimed as SEQ ID NO:
FT 38 in claim 2 of the specification"
FT CDS
FT /*tag= a
FT /product= "Peiwt4NS97 protein /note "CDS does not include
FT start codon"
FT /partial
XX
XX WO200160849-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US0005048.
XX
XX 16-FEB-2000; 2000US-00506286.
XX
XX (UYPI-) UNIV PITTSBURGH.
XX
XX Dowling PW, Youngner JS;
XX
XX WPI; 2001-522584/57.
XX
XX P-PSDB; AAE09028.
XX
XX Novel isolated equine influenza virus (wild-type and cold-adapted)
XX proteins and viruses containing nucleic acid molecules encoding the
XX proteins, which are useful for protecting animals from influenza virus
XX infections.
XX
XX Claim 2; Page 74-75; 172pp; English.
XX
XX The patent discloses cold-adapted equine influenza viruses and
XX reasortant influenza A viruses comprising atleast one genome segment of
XX such an equine influenza virus, wherein the equine influenza virus genome
XX segment confers atleast one identifying phenotype of the cold-adapted
XX equine influenza virus, such as cold adaptation, temperature sensitivity,
XX dominant interference or attenuation. The viruses are useful for
XX protecting animals from diseases caused by influenza viruses. They are
XX also used as vaccines. The present sequence is equine influenza (ei)
XX virus H3N8 neiwt4 (wild type) NS468 DNA encoding Peiwt4NS97 protein
XX
XX Sequence 468 BP; 168 A; 80 C; 98 G; 122 T; 0 U; 0 Other;
```

```
Query Match 42.2%; Score 291.4; DB 4; Length 468;
Best Local Similarity 99.7%; Pred. No. 1.6e-83;
Matches 292; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 398 ACTTTAGTGTGATTTTCGAAAAGGCTGGAGACACTAATACTACTTAGAGCCCTTCAACGGAAG 457
Db 1 ACTTTAGTGTGATTTTCGAAAAGGCTGGAGACACTAATACTACTTAGAGCCCTTCAACGGAAG 60
QY 458 AAGGAGCAGTCGTTGGCGGAAATTTTCCATTGCTTCTCTCCAGGACATACATAATGAGG 517
Db 61 AAGGAGCAGTCGTTGGCGGAAATTTTCCATTGCTTCTCTCCAGGACATACATAATGAGG 120
QY 518 ATGTCAAAAATGCAATTTGGGGTCTCATCGAGGACTTAAATGGAATGATAATACGGTTA 577
Db 121 ATGTCAAAAATGCAATTTGGGGTCTCATCGAGGACTTAAATGGAATGATAATACGGTTA 180
QY 578 GAATCTCTGAAACTCTACAGAGATTCGTTGGAGAGCAGTCATGAGNATGGGAGACCTT 637
Db 181 GAATCTCTGAAACTCTACAGAGATTCGTTGGAGAGCAGTCATGAGNATGGGAGACCTT 240
QY 638 CATTCCTCCAAAGCAGAAACGAAAATGGAGAGAACATTTGAGCCAGAGTT 690
Db 241 CATTCCTCCAAAGCAGAAACGAAAATGGAGAGAACATTTGAGCCAGAGTT 293
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Search completed: March 8, 2006, 00:20:54  
Job time : 434.327 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 00:04:28 ; Search time 3553.19 Seconds  
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Title: US-10-734-373-59

Perfect score: 690

Sequence: 1 atggattccaactgtgtc.....gaacaattgagccagaagtt 690

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_in.\*
- 3: gb\_env.\*
- 4: gb\_cm.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pr.\*
- 9: gb\_ro.\*
- 10: gb\_sta.\*
- 11: gb\_sy.\*
- 12: gb\_tu.\*
- 13: gb\_vl.\*
- 14: gb\_hg.\*
- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	690	100.0	690	6	AR254665	AR254665 Sequence
2	690	100.0	690	6	AR254670	AR254670 Sequence
3	690	100.0	690	6	AR455540	AR455540 Sequence
4	690	100.0	690	6	AR455545	AR455545 Sequence
5	690	100.0	690	6	AR225024	AR225024 Sequence
6	690	100.0	690	6	AR225031	AR225031 Sequence
7	690	100.0	888	6	AR254666	AR254666 Sequence
8	690	100.0	888	6	AR254669	AR254669 Sequence
9	690	100.0	888	6	AR455541	AR455541 Sequence
10	690	100.0	888	6	AR455544	AR455544 Sequence
11	690	100.0	888	6	AR225025	AR225025 Sequence
12	690	100.0	888	6	AR225029	AR225029 Sequence
13	690	100.0	891	6	AR254664	AR254664 Sequence
14	690	100.0	891	6	AR455539	AR455539 Sequence
15	690	100.0	891	6	AR225022	AR225022 Sequence
16	688.4	99.8	838	13	AF001666	AF001666 Influenza
17	688.4	99.8	838	13	AF001668	AF001668 Influenza
18	686.8	99.5	838	13	AF001667	AF001667 Influenza

19	686.8	99.5	838	13	AF001671	AF001671 Influenza
20	686.8	99.5	838	13	AF001673	AF001673 Influenza
21	683.6	99.1	838	13	AF001669	AF001669 Influenza
22	682	98.8	693	6	A52624	A52624 Sequence 6
23	682	98.8	693	13	EIVNS1	X80060 Influenza A
24	682	98.8	890	13	FLANSEQUITE	M80973 Influenza A
25	680.4	98.6	838	13	AF001664	AF001664 Influenza
26	677.2	98.1	838	13	AF001662	AF001662 Influenza
27	677.2	98.1	838	13	AF001670	AF001670 Influenza
28	674	97.7	808	13	IAU49487	U49487 Influenza A
29	674	97.7	890	13	FLANSEOKEN	M80971 Influenza A
30	672.4	97.4	890	13	FLANSEOLON	M80954 Influenza A
31	672.4	97.4	890	13	FLANSEOUNM	M80955 Influenza A
32	670.8	97.2	890	13	FLANSEONY	M80975 Influenza A
33	667.6	96.8	693	13	EIN430785	AJ430785 Influenza
34	667.6	96.8	693	13	AY328471	AJ328471 Influenza
35	667.6	96.8	890	13	AY855345	AY855345 Influenza
36	667.6	96.8	890	13	FLANSEQCOR	M80923 Influenza A
37	667.6	96.8	890	13	FLANSEQSAN	M80972 Influenza A
38	666	96.5	838	13	AF001663	AF001663 Influenza
39	664.4	96.3	808	13	AF001665	AF001665 Influenza
40	664.4	96.3	808	13	IAU49486	U49486 Influenza A
41	662.8	96.1	838	13	AF001672	AF001672 Influenza
42	661.2	95.8	890	13	FLANSEQFON	M80953 Influenza A
43	614.8	89.1	865	13	IAU85376	U85376 Influenza A
44	613.2	88.9	869	13	FLANSMNYA	M25376 Influenza A
45	611.6	88.6	890	13	FLANSMALNY	M80945 Influenza A

#### ALIGNMENTS

RESULT 1  
AR254665 AR254665 690 bp DNA linear PAT 20-DEC-2002  
LOCUS Sequence 52 from patent US 6482414.  
DEFINITION  
ACCESSION AR254665  
VERSION AR254665.1 GI:27303686  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified  
AUTHORS Dowling,P.W. and Youngner,J.S.  
TITLE Cold-adapted equine influenza viruses  
JOURNAL Patent: US 6482414-A 52 19-NOV-2002;  
The University of Pittsburgh-of the Commonwealth System of Higher Education, Pittsburgh, PA

FEATURES  
source  
1..690  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN	Query Match	100.0%;	Score 690;	DB 6;	Length 690;
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QY	1	ATGGATTCCAACACTGTGTCAAGCTTTCAAGTGTAGACTGTTTCTTTGGCATGTCGGCAA	60		
Db	1	ATGGATTCCAACACTGTGTCAAGCTTTCAAGTGTAGACTGTTTCTTTGGCATGTCGGCAA	60		
QY	61	CGATTTCGAGACCAAGAACTGGGTGATGCCCTTCTTCACCGGCTTCGGCGAGACCAG	120		
Db	61	CGATTTCGAGACCAAGAACTGGGTGATGCCCTTCTTCACCGGCTTCGGCGAGACCAG	120		
QY	121	AGTCCCTTAAAGAGAGGTCAGCTTCTTGGTCTGGACATCGAAGACCACTCGTGCA	180		
Db	121	AGTCCCTTAAAGAGAGGTCAGCTTCTTGGTCTGGACATCGAAGACCACTCGTGCA	180		
QY	181	GGAAAGCAGATGTGGAGCGAGATTCTGGAGAGGAGTCTGAGGCACTTAAATGACC	240		
Db	181	GGAAAGCAGATGTGGAGCGAGATTCTGGAGAGGAGTCTGAGGCACTTAAATGACC	240		



181	Qy	GGAAAGCAGATAGTGGAGCAGATTTCTCGAAGAGGAATCAGATGAGGCATTTAAATGACC	240
181	Db	GGAAAGCAGATAGTGGAGCAGATTTCTCGAAGAGGAATCAGATGAGGCATTTAAATGACC	240
241	Qy	ATTGCCCTCTGCTTCCTGCTTCAAGCTCTTAACTGACATGACTCTTGTGATGAGATGTCACAGA	300
241	Db	ATTGCCCTCTGCTTCCTGCTTCAAGCTCTTAACTGACATGACTCTTGTGATGAGATGTCACAGA	300
301	Qy	GACTGGTTCATGCTCATNGCCGACGAGAAAGTAAACGGCTCCCTATCTATATAGAAATGGAC	360
301	Db	GACTGGTTCATGCTCATNGCCGACGAGAAAGTAAACGGCTCCCTATCTATATAGAAATGGAC	360
361	Qy	CAGCAATCATGGATAGAAACATCATATCTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG	420
361	Db	CAGCAATCATGGATAGAAACATCATATCTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG	420
421	Qy	CTGGAGACACTAATACTACTTTAGAGCCCTTCAACGAGAGGAGCAGTCGTTGGCGAAATT	480
421	Db	CTGGAGACACTAATACTACTTTAGAGCCCTTCAACGAGAGGAGCAGTCGTTGGCGAAATT	480
481	Qy	TCACCATTGCCTTCTCTTCTCCAGGACATCATATGAGGATGTCAAAAATGCAATTTGGGGTC	540
481	Db	TCACCATTGCCTTCTCTTCTCCAGGACATCATATGAGGATGTCAAAAATGCAATTTGGGGTC	540
541	Qy	CTCATCGGAGGACTTAAATTGGAAATGATAATACGGTTTAGAACTCTCTGAAACTCTACAGAGA	600
541	Db	CTCATCGGAGGACTTAAATTGGAAATGATAATACGGTTTAGAACTCTCTGAAACTCTACAGAGA	600
601	Qy	TTTCGCTTTGGAGAGCAGTCATGAGAAATGGGAGACCTTCAITCCCTCCAAAGCAGAGAAACGA	660
601	Db	TTTCGCTTTGGAGAGCAGTCATGAGAAATGGGAGACCTTCAITCCCTCCAAAGCAGAGAAACGA	660
661	Qy	AAAAATGGAGAGCAAAATTTGAGCCAGAAGTT	690
661	Db	AAAAATGGAGAGCAAAATTTGAGCCAGAAGTT	690

RESULT 4				
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LOCUS	AR455545	690 bp	DNA	linear
DEFINITION	Sequence 59 from patent US 6685946.			PAT 20-FEB-2004
ACCESSION	AR455545			
VERSION	AR455545.1			
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ORIGIN
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Best Local Similarity 100.0%; Pred.No. 4,3e+191;
Matches 690; Conservative 0; Mismatches 0; Gaps 0;
Indels 0; Gaps 0;

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Db	301	360	420	480	540	600	660	720	780	840	900
Qy	361	420	480	540	600	660	720	780	840	900	960
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Qy	481	540	600	660	720	780	840	900	960	1020	1080
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Qy	541	600	660	720	780	840	900	960	1020	1080	1140
Db	541	600	660	720	780	840	900	960	1020	1080	1140
Qy	601	660	720	780	840	900	960	1020	1080	1140	1200
Db	601	660	720	780	840	900	960	1020	1080	1140	1200
Qy	661	720	780	840	900	960	1020	1080	1140	1200	1260
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	Best Local Similarity	100.0%	Pred. No. 4.3e-191;							
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Db	1	ATGGATTCCAACTGTGTCAAAGCTTTTCAGGTAGACTGTTTCTTTTGGCATGTCGCAAA	60							
QY	61	CGATTGTGACAGCAAAACTGGGTGATGCCCACTTCCTTTGACCGGGTTCGCCGAGACGAG	120							





Query Match		100.0%;	Score 690;	DB 6;	Length 888;
Best Local Similarity		100.0%;	Pred. No. 4.3e-191;		
Matches 690;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY	121	AAGTCCCTAAAAGGAGAGGTAGCCTCTTGGTCTGGACATCGAAACAGCCACTCTG	180		
DB	145	AAGTCCCTAAAAGGAGAGGTAGCCTCTTGGTCTGGACATCGAAACAGCCACTCTG	204		
QY	181	GGAAAGCAGATAGTGGAGCAGATTTCTGGAAGAGGAATCAGATGAGGCACCTTAAATG	240		
DB	205	GGAAAGCAGATAGTGGAGCAGATTTCTGGAAGAGGAATCAGATGAGGCACCTTAAATG	264		
QY	241	ATTGCTCTGTTCTGCTTCACTGCTTAACTGACATGACTCTTATGATGAGATGTCA	300		
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QY	361	CAGCAATCATGATGAAGAACATCATACTTAAAGCAAACTTTAGTGTGATTTTGA	420		
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QY	541	CTCATCGGAGACTTAAATGGAATGATAATACGGTTAGAACTCTGAAACTCTAC	600		
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LOCUS  
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AR45544  
AR45544.1 GI:42690364  
DEFINITION  
Accession  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 888)  
Dowling, P.W. and Youngner, J.S.  
Cold-adapted equine influenza viruses  
Patent: US 6685946-A 57 03-FEB-2004;  
The University of Pittsburgh-of the Commonwealth System of Higher  
Education; Pittsburgh, PA  
Location/Qualifiers  
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Sequence 35 from Patent WO0160849.  
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KEYWORDS  
SOURCE  
ORGANISM  
Equine influenza virus H3N8  
Equine influenza virus H3N8  
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
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REFERENCE  
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Dowling, P.W. and Youngner, J.S.  
Cold-adapted equine influenza viruses  
Patent: WO 0160849-A 35 23-AUG-2001;  
UNIV. OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION  
(US)

FEATURES

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Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 4.3e-191;  
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12

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ACCESSION  
AX225029.1 GI:15555102  
VERSION  
EQUINE influenza virus H3N8  
KEYWORDS  
EQUINE influenza virus H3N8  
SOURCE  
VIRUSES; ssRNA negative-strand viruses; Orthomyxoviridae;  
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REFERENCE  
1 Dowling, P.W. and Youngner, J.S.

TITLE

JOURNAL  
Cold-adapted equine influenza viruses  
Patent: WO 0160849-A 39 23-AUG-2001;  
UNIV. OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION  
(US)

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ORIGIN

Query Match 100.0%; Score 690; DB 6; Length 888;  
Best Local Similarity 100.0%; Pred. No. 4.3e-191;  
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGATTCCACACTGTGTCAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 60  
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LOCUS AR254664 891 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 50 from patent US 6482414.  
ACCESSION AR254664  
VERSION AR254664.1 GI:27303685  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 891)  
AUTHORS Dowling, P.W. and Youngner, J.S.  
TITLE Cold-adapted equine influenza viruses  
JOURNAL Patent: US 6482414-A 50 19-NOV-2002;  
The University of Pittsburgh-of the Commonwealth System of Higher  
Education; Pittsburgh, PA  
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Query Match 100.0%; Score 690; DB 6; Length 891;  
Best Local Similarity 100.0%; Pred. No. 4.3e-191; Indels 0; Gaps 0;  
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTCCAAACACCTGTGCTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAA 60  
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RESULT 14  
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DEFINITION Sequence 50 from patent US 6685946.  
ACCESSION AR455539  
VERSION AR455539.1 GI:42690359  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 891)  
AUTHORS Dowling, P.W. and Youngner, J.S.  
TITLE Cold-adapted equine influenza viruses  
JOURNAL Patent: US 6685946-A 50 03-FEB-2004;  
The University of Pittsburgh-of the Commonwealth System of Higher  
Education; Pittsburgh, PA  
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Best Local Similarity 100.0%; Pred. No. 4.3e-191; Indels 0; Gaps 0;  
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AX225022
LOCUS AX225022
DEFINITION Sequence 32 from Patent WO0160849.
ACCESSION AX225022
VERSION AX225022.1 GI:15555095
KEYWORDS Equine influenza virus H3N8
SOURCE Equine influenza virus H3N8
ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
REFERENCE
AUTHORS Dowling, P.W. and Youngner, J.S.
TITLES Cold-adapted equine influenza viruses
JOURNAL Patent: WO 0160849-A 32 23-AUG-2001;
UNIV. OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION
(US)
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.3e-191;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Maximum DB seq length: 2000000000

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Listing first 45 summaries

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#### SUMMARIES

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4	75.5	6.4	818	7 US-11-087-099-12309	Sequence 12309, A
5	75.5	6.4	2671	6 US-10-876-787-6	Sequence 6, Appli
6	75	6.4	784	6 US-10-873-528-36	Sequence 36, Appl
7	74	6.3	485	7 US-11-087-099-9751	Sequence 9751, Ap
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9	74	6.3	589	6 US-10-821-234-1494	Sequence 1494, Ap
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12	73.5	6.2	1372	7 US-11-087-099-3054	Sequence 3054, Ap
13	73	6.2	468	7 US-11-124-367A-474	Sequence 474, App
14	73	6.2	821	7 US-11-124-367A-473	Sequence 473, App
15	72.5	6.2	427	6 US-10-467-657-4384	Sequence 4384, Ap
16	72.5	6.2	1674	7 US-11-231-599-55	Sequence 55, Appl
17	72	6.1	917	7 US-11-169-041-145	Sequence 145, App
18	72	6.1	1285	7 US-11-206-071-2	Sequence 2, Appli
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23	71.5	6.1	311	7 US-11-228-875-5	Sequence 5, Appli
24	71.5	6.1	263	7 US-11-087-099-6054	Sequence 6054, Ap
25	71.5	6.1	517	7 US-11-169-041-160	Sequence 160, App

26 71 6.0 454 7 US-11-087-099-4144 Sequence 4144, Ap  
27 71 6.0 494 6 US-10-934-944-236 Sequence 236, App  
28 71 6.0 494 7 US-11-116-881A-245 Sequence 245, App  
29 71 6.0 551 7 US-11-156-953-2 Sequence 2, Appli  
30 71 6.0 1131 7 US-11-072-512-2866 Sequence 2866, Ap  
31 6.0 1278 6 US-10-995-561-952 Sequence 952, App  
32 70.5 6.0 391 7 US-11-087-099-10561 Sequence 10561, A  
33 70.5 6.0 466 7 US-11-074-176-58 Sequence 58, Appl  
34 70.5 6.0 473 7 US-11-152-366-32 Sequence 32, Appl  
35 70.5 6.0 539 6 US-10-821-234-1567 Sequence 1567, Ap  
36 70.5 6.0 708 7 US-11-196-475-76 Sequence 76, Appl  
37 70.5 6.0 769 7 US-11-087-099-4295 Sequence 4295, Ap  
38 70 5.9 326 7 US-11-087-099-9424 Sequence 9424, Ap  
39 70 5.9 528 6 US-10-858-730-88 Sequence 88, Appl  
40 70 5.3 1112 7 US-11-087-099-10149 Sequence 10149, A  
41 70 5.3 1316 7 US-11-091-643-4 Sequence 4, Appli  
42 69.5 5.9 288 6 US-10-467-657-1682 Sequence 1682, Ap  
43 69.5 5.9 412 6 US-10-330-773-6 Sequence 6, Appli  
44 69.5 5.9 487 7 US-11-227-881-1 Sequence 1, Appli  
45 69.5 5.9 1006 6 US-10-467-657-8400 Sequence 8400, Ap

#### ALIGNMENTS

RESULT 1  
US-11-087-099-5013  
; Sequence 5013, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 5013  
; LENGTH: 1035  
; TYPE: PRT  
; ORGANISM: Pichia pastoris  
US-11-087-099-5013

Query Match 7.2%; Score 84.5; DB 7; Length 1035;  
Best Local Similarity 24.8%; Pred. No. 3.6; Indels 33; Gaps 7;

Matches 37; Conservative 32; Mismatches 47; Indels 33; Gaps 7;

QY 32 FLDRLRRDQKSLKRGSTL-----GLDIETATAGQIVQVEILEESDEALKMTIASVP 85

DB 96 FLDLLKYDCPSLGHRIHYMLQLLEFKLQVEKYREANEKISRLYQVDDG---RRSIAAAE 152

QY 86 ASRYLTDM-----TLDEMGRDFML--MPKQKVTGSLCIRMDQAIMDK 126

DB 153 GKGVESDMKIHLMQKALKNYHVDVHNIDEVARDTEVMTFRKPLSGTSLITIN-SIRD- 210

QY 127 NIILKANFSVIFERLETILLRAFTEGA 155

DB 211 --ILHVS-SIFSKKLETIVSIRLMTVEKA 236

#### RESULT 2

US-11-087-099-3833  
; Sequence 3833, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 3833  
; LENGTH: 313  
; TYPE: PRT

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; ORGANISM: Vibrio parahaemolyticus RIMD 2210633
US-11-087-099-3833
Query Match
Best Local Similarity 7.0%; Score 82; DB 7; Length 313;
Matches 40; Conservative 28; Mismatches 41; Indels 74; Gaps 8;
QY 38 RDQSLKRGSTGLGDIETATRAKQIVQIILEESDEALKMTIASVPASRYLTD-----92
Db 18 REQMSDELQQSILA-DLEAAVKAGHQILEQ-----GGEALDAVVAV---KVLDESFPNF 68
QY 93 -----MTLDEMSRDWFMLMPKQKVTGSLCIRMDQAIWD-KNIIKANFSVIFERLETLI 145
Db 69 AGKGSVLTHNEM-----VEMDASVMDGRNL-----93
QY 146 LLRAFTTEGAVGEISPLSPGHTNEDVKNAGIVGLGGLKNDNTVRISETLORFPAWRS 205
Db 94 -----AGAVAGV-----RHKNPIELARDVMLRSNHYLLVGEAEKFAFEQ 135
QY 206 SHE 208
Db 136 GHQ 138
RESULT 3
US-11-087-099-8680
; Sequence 8680, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8680
; LENGTH: 1115
; TYPE: PRT
; ORGANISM: Ipomoea nil
US-11-087-099-8680
Query Match
Best Local Similarity 6.7%; Score 79.5; DB 7; Length 1115;
Matches 60; Conservative 39; Mismatches 92; Indels 99; Gaps 13;
QY 14 FLWHVRKR---PADQLGDAPFLDRRLRRDQSLKGRG-----SLQIGENYMKSVSSPQNDSDGVRFYEL 595
Db 538 FLEVVKRSPLWEDSEINATHSLQLMRD--SLQIGENYMKSVSSPQNDSDGVRFYEL 595
QY 48 STIGLD-----TETAT-----RAGKOIVQIILEESD 74
Db 596 SSNALELVETATVPFGVDSGLINGWNAKIAELTGLQANVAIGKLIIDVTHEDSH 655
QY 75 EALK-----MTIASVPASRYLTDMLDEMSRDWFMLMPKQKVTGSL 115
Db 656 ETKALMCRALQGEDRNVKLFKGNHPTKEVYLVNACTSRDY-----KNDIIG-V 709
QY 116 C-----IRMDQIMDKNIIKANFSVIFERLETLILLRAFTERGAVVGE-ISPLSPGPH 169
Db 710 CFVGQDITPEKAVMDKVRLOQGYEALIQSLNPLPIPFASDENACCSEWNAAMERLTGL 769
QY 170 TNDV--KNAIGVLGG---LKWNDNTVRISETLORFPAWRSSEHNGRPSF 214
Db 770 VKCEVIGKELPGEIPGGLCRLLKGODALTKFMILL--YQGISGHDTEKLSF 817
RESULT 4
US-11-087-099-12309
; Sequence 12309, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12309
; LENGTH: 818
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-11-087-099-12309
Query Match
Best Local Similarity 6.4%; Score 75.5; DB 7; Length 818;
Matches 46; Conservative 31; Mismatches 77; Indels 67; Gaps 10;
QY 21 RP-ADQSLGDAPFLDRRLRRDQKS-----LKGRGSLTGLDIETATRAKQIVQIILEES 71
Db 521 RFGVEKPLGDAGTAETAETARKSDIVLLLVGRGEWDTEGLDIPMRLPGEQ--EELIE- 577
QY 72 ESDALKMTIASVPASRYLTDMLDEMSRDWF-----MLMPKQKVTGSLCIRMDQAI 123
Db 578 -----AVARETNPNVVVLQTGGPIEMPWLKRVAVLQMWYFQELGNALA-----622
QY 124 MDKNIIKANFSVIFERLETLILL-----RAFTTEGAVVGEISPLSPGHTNEDVKNAI 178
Db 623 -----DVLPGDVEPAGRLPQTFFPKALTDNSAITDDPSIYFGODGH-----VRYAE 667
QY 179 GVLIGGLKNDNTVRISETL-----ORFAWRSSHENG 210
Db 668 GIFVG---YRHDTREIEPLFPFGGLGYTRFTWGAPOQLSG 705
RESULT 5
US-10-876-787-6
; Sequence 6, Application US/10876787
; Publication No. US20050287535A1
; GENERAL INFORMATION:
; APPLICANT: McGraith, Kevin P.
; APPLICANT: Kimberly-Clark Worldwide, Inc.
; TITLE OF INVENTION: BIOMARKERS FOR WOUND HEALING
; FILE REFERENCE: 1443.156U1
; CURRENT APPLICATION NUMBER: US/10/876,787
; CURRENT FILING DATE: 2004-06-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2671
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-876-787-6
Query Match
Best Local Similarity 6.4%; Score 75.5; DB 6; Length 2671;
Matches 48; Conservative 30; Mismatches 70; Indels 63; Gaps 10;
QY 17 HVKRFADQE-----LGDAPFLDRRLRRDQSLKGR-----GSTLGLDITAT 58
Db 1790 HDKMKRAQQETKSTVAVNNDLGSQPHEDREFVD-PTTKGRVASIFSISRSYSIGPSL 1848
QY 59 RAGKOIVQIILEESDEALKMTIASVPASRYLTDMLDEMSRDWFMLMPKQKVTGSLCIR 118
Db 1849 RRGHEVSERV---QSSEMTGTVLIMQPLRLPL-OLLCENHNRD-----1887
QY 119 MDQAIMDKNIIKANFSVIFERLETLILLRAFTERGAVVGEISPLSPGHTNEDVKNAI 178
Db 1888 LQNFRLQCN--NKTNYNLVCTLOPLDIMCGSTTGG-----LGLLGLYINED---NV 1934
QY 179 GVLIGGLKNDNTVRISETLORFPAWRSSEH 209
Db 1935 GLVITQL-----ETLTYEQCPCHEN 1955
RESULT 6
US-10-873-528-36
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; Sequence 36, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR FILING DATE: 2004-06-23
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 36
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-36

Query Match
Best Local Similarity 6.4%; Score 75; DB 6; Length 784;
Matches 47; Conservative 30; Mismatches 71; Indels 60; Gaps 9;

QY 1 MGSNTVSPQVDCFLMVRKRFADQELG---DAPFLRLRRDQSKLGRGSLGLDIETA 57
DB 102 IDGDTVEV-----VIKKVADRNRKGTAAEAKIIDILEHSLTTVVGQ---IVLDDQKP 149

QY 58 TRAG-----KQIVEQ-----ILEEESDEALKMTIASVPASRYLTDMTLDMSRDWFL 105
DB 150 KYAGYIRSKNOKISQPIYVKKPKLEGTEVLKVIDKYPSKKH-----DFFVA 198

QY 106 MPKQKVTGSLCIRMDQAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEIS 165
DB 199 SVLDDVGHSTVDGID-----VLEVESMDIVSEFPE--AVVKEAESVPD 240

QY 166 LPQHTNE-----DVKNAGVLIGGLKWN 189
DB 241 APSQDMEGRLDRDEITFTIDGADAKD 268

RESULT 7
US-11-087-099-9751
; Sequence 9751, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9751
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Glycine max
US-11-087-099-9751

Query Match
Best Local Similarity 6.3%; Score 74; DB 7; Length 485;
Matches 49; Conservative 42; Mismatches 99; Indels 58; Gaps 12;

QY 8 SFQVDCFLMH-----VRKRFADQELGDAPFLRLRRDQ-----KSLKGRGSLTG- 51
DB 4 AFQKSWIEHTTIDSVESMMLDSNASD---LDKEERPEVLSLLPPYEGKSVVELGAGIG 60

QY 52 LDLETATRAKQIVQEULEE--ESDEAL-----KMTIASVPA-SRYLTDMTLDMSRD 101
DB 61 FTVELAKKAGQLAVDFIESAIKKNESINGHHKVKFWCADVTSPLNIYISEGSVDLIFSN 120
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```
QY 102 WFMLMPKQKVTGSLCIRMDQAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEIS 161
DB 121 WLLMYLSDKEVENLAARMIK-----WLKVGGVVFFRE-----SCFHQSGDSKKRYN 166
QY 162 PL-----PSL-----PGHTNEDVKNAGVLIGGLKWNNDTVRISETLQRFW-----RSS 206
DB 167 PTHYREPRFYTKVFKCHECHISDDTRNSFELSLVGCKICGAYVRNKNQNOICWLKMKVRSQ 226
QY 207 HENGRRPSF 214
DB 227 DDRGFQRF 234

RESULT 8
US-11-072-512-2447
; Sequence 2447, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR FILING DATE: 2005-03-07
; PRIOR FILING DATE: 2002-01-25
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2447
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2447

Query Match
Best Local Similarity 6.3%; Score 74; DB 7; Length 509;
Matches 47; Conservative 27; Mismatches 78; Indels 50; Gaps 10;

QY 20 KRFADQELG-----APFLRLRRDQSKLGRGSLGLDIETATRAKQIV 65
DB 102 RRAAASKLGEPAKVLDELNVKSEIIPMFNSLASDEQD-----SVRLLAVEACVN-----I 151
QY 66 EQILEEESDEALKMTIASVPASRYLTDMTLDMSRDWFLMPK---KQVTGSLCIRMDQ 121
DB 152 AQLLPQDEALVN-----PTLRQAAE---DKSVRVRYMVADKFTTELQKAVGPEITKTDL 203
QY 122 AIMDKNIILKANFSV-----IFERLETLILLRAFTTEGAVVGEISL-PLSLPGHTNED 173
DB 204 VPAFQNLKQCEAEVRAAASHKVGFECN---LSADCENNVMSQILPCIKELVSDANQH 260
QY 174 VKNAIGVLIGGLK---WNNDTV 192
DB 261 VKSALASVIMGLSPILGKONTI 282
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RESULT 9  
US-10-821-234-1494  
; Sequence 1494, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclerapsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; PRIOR FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: Pf Seq\_genes Version 1.0  
; SEQ ID NO 1494  
; LENGTH: 589  
; TYPE: PRP  
; ORGANISM: Homo sapiens  
US-10-821-234-1494

Query Match 6.3%; Score 74; DB 6; Length 589;  
Best Local Similarity 23.3%; Pred. No. 19;  
Matches 47; Conservative 27; Mismatches 78; Indels 50; Gaps 10;  
QY 20 KRPADQELG-----APFLRLRRDQKSLKRGSTGLGLDIETATRAGQIV 65  
DB 182 RRAAASKLGEFAKVLSDNYKSEIIPFNSNLASDEQ-----SVRLVAEACVN-----I 231  
QY 66 EQILEESDEALKMTIASVPASRYLTDMTLDEMGRDFMLMPK---QKVTGSLCIRMDQ 121  
DB 232 AOLLPQEDLEALVM-----PTLRQAAE---DKSWRVYVMVADKFTBLQKAVGPEITKTDL 283  
QY 122 AIMDKNIILKANFSV-----IFERLETLILLRAFTTEGAVVGEISP-LPSLPQHTNED 173  
DB 284 VPAFQNLAKDCEAEVRAASHKVFECEN---LSADCRENVMSQILPCIKELVSDANQH 340  
QY 174 VKNAIGVLIGLK---WMDNTV 192  
DB 341 VKSALASVIMGLSPILGKDNTI 362

RESULT 10  
US-10-467-657-5508  
; Sequence 5508, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; APPLICANT: FONTANA, Maria Rita  
; APPLICANT: PIZZA, Mariagrazia  
; APPLICANT: MASIGNANI, Vega  
; APPLICANT: MONACI, Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; PRIOR FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 5508  
; LENGTH: 943  
; TYPE: PRP  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-5508

Query Match 6.2%; Score 73.5; DB 6; Length 943;  
Best Local Similarity 23.1%; Pred. No. 41;  
Matches 39; Conservative 29; Mismatches 59; Indels 43; Gaps 8;

QY 34 DRLRRDQ-----KSLKRGSTGLGLDIETATRAGQIVQILEESDEALKMTIASVPASRY 89  
DB 299 DRRNRDDEGQGRNAKGGAKGGRDRNRNARNGD---ERVGGKGGKGLKLE-PNQHAFQA 354  
QY 90 LTDMTLDEMGRDFMLMPKQKVTGSLC-----IRMDQAIMDKNIILKANFSVIPERLE 142  
DB 355 PTEPVRHE-----VLVPETITVADLAHKMAVGVEMVKALMKGMVVTINOSI--DQDT 406  
QY 143 TLILLR-----AFTTEGAVVGEISPLPSLP-----GHTN 171  
DB 407 ALIVVKKLGHGKPRAADPPEAFLEGGAEEAEALPPPVVTVVGHVD 455  
RESULT 11  
US-11-052-554A-250  
; Sequence 250, Application US/11052554A  
; Publication No. US20050288666A1  
; GENERAL INFORMATION:  
; APPLICANT: Sachdeva, et al.  
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE  
; FILE REFERENCE: 30853/40359A  
; CURRENT APPLICATION NUMBER: US/11/052,554A  
; PRIOR FILING DATE: 2005-02-07  
; PRIOR APPLICATION NUMBER: US 60/589,227  
; PRIOR FILING DATE: 2004-07-20  
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004  
; PRIOR FILING DATE: 2004-02-06  
; NUMBER OF SEQ ID NOS: 763  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 250  
; LENGTH: 1037  
; TYPE: PRP  
; ORGANISM: Neisseria meningitidis 22491  
US-11-052-554A-250

Query Match 6.2%; Score 73.5; DB 7; Length 1037;  
Best Local Similarity 23.6%; Pred. No. 46;  
Matches 51; Conservative 32; Mismatches 70; Indels 63; Gaps 12;  
QY 16 WHVKRRF-ADQELGDAPFLRLRRDQKSLKRGSTL-----GL----DIETA 57  
DB 760 WTVRTIFQGTKPITSAPAISSQLKDKRVVIFGTGSLSEDDVLSTDEQHIYGFNDNTNG 819  
QY 58 TR---AGKQIVQILEESDEALKMTIASVPASRYLTDMTLDEMGRD--WFM-LMPKQV 111  
DB 820 TAQEGKGLLEQKLEEN-----KTLFLTDYKRSQSGSGDKGVVVKLQKQV 867  
QY 112 TGSCLIRMDQAIMDKNIILKANFSVIPE-----RLETLILLRAFTTEGAVVGEISPLP 164  
DB 868 T-----VKPTVLRFAFTIHKYTGNDKCGAETAL-LGINTADGGKLTAKSARP 915  
QY 165 SLPGHTNE-----DVKNAGI--VLIGLKWNDTV 192  
DB 916 IVPAAANSKVAQYSGDKTSSGKSIPIGOMKDGTV 951

RESULT 12  
US-11-087-099-3054  
; Sequence 3054, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 3054  
; LENGTH: 1372  
; TYPE: PRP  
; ORGANISM: Cercospora zeae-maydis  
US-11-087-099-3054



Db 228 KLKWA---DRLPRILY--YKQEGEIVSRDDPQGRVSIFDRLP-----QASSRWVAIGR 277

Oy 185 LKWNDNTVRI-----SETLQRFAPWRSSHENGREPF 214

Db 278 LDINTSGLLILTTSGELVQRF-----HPSF 303

Search completed: March 7, 2006, 19:26:00  
Job time : 21 secs



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OM protein - protein search, using sw model

Run on: March 7, 2006, 19:22:04 ; Search time 166 Seconds  
(without alignments)  
578.920 Million cell updates/sec

Title: US-10-734-373-58  
Perfect score: 1178  
Sequence: 1 MDSNTVSSFDVDFLWHYRK.....RPSFPKOKRMERTIEPEV 230

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:\*

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2: /cgn2\_6/ptodata/1/pubaa/US08\_PUBCOMB.pep.\*  
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6: /cgn2\_6/ptodata/1/pubaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1178	100.0	230	4	US-10-065-133A-58
3	1178	100.0	230	4	US-10-734-373-51
4	1178	100.0	230	4	US-10-734-373-58
5	1178	100.0	230	5	US-10-181-585B-33
6	1178	100.0	230	5	US-10-181-585B-40
7	1061	90.1	238	5	US-10-654-737-3
8	1055	89.6	237	4	US-10-381-530-17
9	1052	89.3	230	5	US-10-654-737-5
10	488	41.4	97	4	US-10-065-133A-55
11	488	41.4	97	4	US-10-734-373-55
12	488	41.4	97	5	US-10-181-585B-37
13	400	34.0	344	3	US-09-822-827-973
14	400	34.0	344	3	US-09-895-793-973
15	387	32.9	312	4	US-10-312-089-1
16	385.5	32.7	312	4	US-10-312-089-3
17	385	32.7	282	4	US-10-226-872-10
18	385	32.7	282	4	US-10-473-127-1114
19	384	32.6	403	5	US-10-650-608-10
20	100	8.5	478	4	US-10-369-493-501
21	93	7.9	477	4	US-10-369-493-21219
22	93	7.9	1873	4	US-10-087-192-666
23	90	7.6	233	4	US-10-424-599-213467
24	89.5	7.6	956	5	US-10-719-993-597
25	89.5	7.6	1876	3	US-09-839-479-70
26	89.5	7.6	1876	4	US-10-376-537-71
27	89.5	7.6	1876	4	US-10-702-148-70

28	89	7.6	1448	4	US-10-282-122A-66468	Sequence 66468, A
29	87.5	7.4	842	4	US-10-820-307-3	Sequence 3, Appli
30	87.5	7.4	844	3	US-09-866-020-30	Sequence 30, Appl
31	87.5	7.4	844	3	US-09-813-148-4	Sequence 4, Appli
32	87.5	7.4	844	3	US-09-810-796-14	Sequence 14, Appl
33	87.5	7.4	844	4	US-10-295-027-282	Sequence 282, App
34	87.5	7.4	844	4	US-10-661-629-4	Sequence 4, Appli
35	87.5	7.4	844	5	US-10-643-795A-152	Sequence 152, App
36	87.5	7.4	844	5	US-10-850-928-34	Sequence 34, Appl
37	87.5	7.4	844	5	US-10-948-493-29	Sequence 29, Appl
38	87.5	7.4	844	5	US-10-948-518-152	Sequence 152, App
39	87.5	7.4	844	5	US-10-482-83A-161	Sequence 161, App
40	87.5	7.4	844	5	US-10-287-436A-601	Sequence 601, App
41	87.5	7.4	872	4	US-10-345-680-17	Sequence 17, Appli
42	87.5	7.4	872	4	US-10-096-578-2	Sequence 2, Appli
43	87.5	7.4	872	4	US-10-820-307-2	Sequence 2, Appli
44	87.5	7.4	872	4	US-10-744-796-7	Sequence 7, Appli
45	87.5	7.4	912	5	US-10-450-763-41003	Sequence 41003, A

## ALIGNMENTS

RESULT 1  
US-10-065-133A-51  
; Sequence 51, Application US/100651133A  
; Publication No. US20030199074A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2-1  
; CURRENT APPLICATION NUMBER: US/10/065,133A  
; PRIOR FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; PRIOR APPLICATION NUMBER: 09/133,921  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 51:  
; LENGTH: 230  
; TYPE: PRT  
; ORGANISM: Equine influenza virus H3N8  
US-10-065-133A-51

Query Match 100.0%; Score 1178; DB 4; Length 230;  
Best Local Similarity 100.0%; Pred. No. 4.1e-116;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDSNTVSSFDVDFLWHYRKRFADQELGDPAPFLDLRRDQKSLKGRGSLGDIETATRA	60
DB	1	MDSNTVSSFDVDFLWHYRKRFADQELGDPAPFLDLRRDQKSLKGRGSLGDIETATRA	60
QY	61	GKQIVQEILLESDEALKMTIASVPASRYLTDMTIDMSRDWFMPLPKOKVTGSLCIRMD	120
DB	61	GKQIVQEILLESDEALKMTIASVPASRYLTDMTIDMSRDWFMPLPKOKVTGSLCIRMD	120
QY	121	QALMDKNITLKANSVIFERLETLILRAFTSEGAVVGEISPLPSLPGHNTDVKNAIGV	180
DB	121	QALMDKNITLKANSVIFERLETLILRAFTSEGAVVGEISPLPSLPGHNTDVKNAIGV	180
QY	181	LIGLKWNDNVTIRSETLQFAWRSSHENGSRPSFPKOKRMERTIEPEV	230
DB	181	LIGLKWNDNVTIRSETLQFAWRSSHENGSRPSFPKOKRMERTIEPEV	230

RESULT 2  
US-10-065-133A-58  
; Sequence 58, Application US/100651133A  
; Publication No. US20030199074A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.

```

; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 59
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
; US-10-065-133A-58

Query Match      100.0%; Score 1178; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 4, 1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLWHVRKFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Db 1 MDSNTVSSFOVDCFLWHVRKFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60

Qy 61 GKQIVEQILLESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILLESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120

Qy 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVGVEISPLPSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVGVEISPLPSLPGHTNEDVKNAGV 180

Qy 181 LIGGLKWNNDTVRISETLQRFAMRSSHENGSRFPFPKQKRMERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLQRFAMRSSHENGSRFPFPKQKRMERTIEPEV 230

```

## RESULT 3

```

US-10-734-373-51
; Sequence 51, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
; US-10-734-373-51

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Query Match      100.0%; Score 1178; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 4, 1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLWHVRKFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Db 1 MDSNTVSSFOVDCFLWHVRKFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60

Qy 61 GKQIVEQILLESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILLESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120

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Qy 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVGVEISPLPSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVGVEISPLPSLPGHTNEDVKNAGV 180

Qy 181 LIGGLKWNNDTVRISETLQRFAMRSSHENGSRFPFPKQKRMERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLQRFAMRSSHENGSRFPFPKQKRMERTIEPEV 230

```

## RESULT 4

```

US-10-734-373-58
; Sequence 58, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
; US-10-734-373-58

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Query Match      100.0%; Score 1178; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 4, 1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLWHVRKFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Db 1 MDSNTVSSFOVDCFLWHVRKFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60

Qy 61 GKQIVEQILLESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILLESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120

Qy 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVGVEISPLPSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVGVEISPLPSLPGHTNEDVKNAGV 180

Qy 181 LIGGLKWNNDTVRISETLQRFAMRSSHENGSRFPFPKQKRMERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLQRFAMRSSHENGSRFPFPKQKRMERTIEPEV 230

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## RESULT 5

```

US-10-181-585B-33
; Sequence 33, Application US/10181585B
; Publication No. US20050175985A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System
; APPLICANT: of Higher Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C3-PUS
; CURRENT APPLICATION NUMBER: US/10/181,585B
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: PCT/US01/05048
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/506,286
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33

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; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-181-585B-33

Query Match 100.0%; Score 1178; DB 5; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLMHWKRPADQELGDAFLDLRLRRDQSKLGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFOVDCFLMHWKRPADQELGDAFLDLRLRRDQSKLGRGSLGLDIETATRA 60
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLDTMTLDEMSEDFWMLMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQILEESDEALKMTIASVPASRYLDTMTLDEMSEDFWMLMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTGAVVGEISPLSLPGHNTNEDVKNAIGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTGAVVGEISPLSLPGHNTNEDVKNAIGV 180
QY 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPFPKQKRWERTIEPEV 230
DB 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPFPKQKRWERTIEPEV 230

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## RESULT 6

```

US-10-181-585B-40
; Sequence 40, Application US/10181585B
; Publication No. US20050175985A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C3-PUS
; CURRENT APPLICATION NUMBER: US/10/181.585B
; PRIOR FILING DATE: 2003-12-08
; PRIOR FILING DATE: PCT/US01/05048
; PRIOR FILING DATE: 2001-02-16
; PRIOR FILING DATE: 09/506,286
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 40
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-181-585B-40

Query Match 100.0%; Score 1178; DB 5; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLMHWKRPADQELGDAFLDLRLRRDQSKLGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFOVDCFLMHWKRPADQELGDAFLDLRLRRDQSKLGRGSLGLDIETATRA 60
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLDTMTLDEMSEDFWMLMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQILEESDEALKMTIASVPASRYLDTMTLDEMSEDFWMLMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTGAVVGEISPLSLPGHNTNEDVKNAIGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTGAVVGEISPLSLPGHNTNEDVKNAIGV 180
QY 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPFPKQKRWERTIEPEV 230
DB 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPFPKQKRWERTIEPEV 230

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## RESULT 7

```

US-10-654-737-3
; Sequence 3, Application US/10654737
; Publication No. US20050054846A1
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital
; APPLICANT: Webster, Robert G
; APPLICANT: Webby, Richard J
; APPLICANT: Ozaki, Hiroichi
; TITLE OF INVENTION: Improved Method for Generating Influenza Viruses and Vaccines
; FILE REFERENCE: SJ-02-0016
; CURRENT APPLICATION NUMBER: US/10/654,737
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Influenza A virus
US-10-654-737-3

Query Match 90.1%; Score 1061; DB 5; Length 238;
Best Local Similarity 88.7%; Pred. No. 1.1e-103;
Matches 204; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLMHWKRPADQELGDAFLDLRLRRDQSKLGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFOVDCFLMHWKRPADQELGDAFLDLRLRRDQSKLGRGSLGLDIETATRA 60
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLDTMTLDEMSEDFWMLMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQILEESDEALKMTIASVPASRYLDTMTLDEMSEDFWMLMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTGAVVGEISPLSLPGHNTNEDVKNAIGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTGAVVGEISPLSLPGHNTNEDVKNAIGV 180
QY 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPFPKQKRWERTIEPEV 230
DB 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPFPKQKRWERTIEPEV 230

RESULT 8
US-10-381-530-17
; Sequence 17, Application US/10381530
; Publication No. US20040137013A1
; GENERAL INFORMATION:
; APPLICANT: KATINGER, Hermann
; APPLICANT: EGOROV, Andre
; APPLICANT: FERKO, Boris
; APPLICANT: ROMANOVA, Julia
; APPLICANT: KATINGER, Dietmar
; TITLE OF INVENTION: LIVE VACCINE AND METHOD OF MANUFACTURE
; FILE REFERENCE: P/167-134
; CURRENT APPLICATION NUMBER: US/10/381,530
; CURRENT FILING DATE: 2003-11-24
; PRIOR FILING DATE: PCT/EP01/11087
; PRIOR FILING DATE: 2001-09-25
; PRIOR FILING DATE: 00120896.6
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 17
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Influenza virus A/Singapore/1/57/ca
US-10-381-530-17

Query Match 89.6%; Score 1055; DB 4; Length 237;
Best Local Similarity 87.8%; Pred. No. 4.7e-103;
Matches 202; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLMHWKRPADQELGDAFLDLRLRRDQSKLGRGSLGLDIETATRA 60

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Db 1 MDNVTSSFOVDCFLMHWVRKQVADQELGDPFLDLRLDQKSLRGSGTLGNIETATRV 60
Qy 61 GKQIVEOILLESDEALKMTIASVPASRYLTDMTLDMSRDWFLMPKOKVTGSLCIRMD 120
Db 61 GKQIVERILKESDEALKMTIASVPASRYLTDMTLTIEMSDKDFWFLMPKOKVSGPLCIRMD 120
Qy 121 QAIMDKNIILKANFSVIPERLETLILLRAFTTEGAVGEISPLPSLPGHTNEDVKNAGIV 180
Db 121 QAIMDKNIILKANFSVIPDRLETLILLRAFTTEGAVGEISPLPSLPGHTNEDVKNAGIV 180
Qy 181 LIGGLKWNNDTVRISETLQRFAPWRSSHENGSRPSPPKOKRMERTIEPEV 230
Db 181 LIGGLEWNNNTVRVSKTLQRFAPWRSSNENGRPPLTPKOKRMARTIRSKV 230

RESULT 9
US-10-654-737-5
; Sequence 55, Application US/10654737
; Publication No. US20050054846A1
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital
; APPLICANT: Webster, Robert G
; APPLICANT: Webby, Richard J
; APPLICANT: Ozaki, Hiroichi
; TITLE OF INVENTION: Improved Method for Generating Influenza Viruses and Vaccines
; FILE REFERENCE: SJ-02-0016
; CURRENT APPLICATION NUMBER: US/10/654,737
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Influenza A virus
US-10-654-737-5

Query Match 89.3%; Score 1052; DB 5; Length 230;
Best Local Similarity 87.8%; Pred. No. 9.3e-103; Indels 0; Gaps 0;
Matches 202; Conservative 16; Mismatches 12;

Qy 1 MDNVTSSFOVDCFLMHWVRKQVADQELGDPFLDLRLDQKSLRGSGTLGNIETATRA 60
Db 1 MDNVTSSFOVDCFLMHWVRKQVADQELGDPFLDLRLDQKSLRGSGTLGNIETATRA 60
Qy 61 GKQIVEOILLESDEALKMTIASVPASRYLTDMTLDMSRDWFLMPKOKVTGSLCIRMD 120
Db 61 GKQIVERILKESDEALKMTIASVPASRYLTDMTLTIEMSDKDFWFLMPKOKVAGPLCIRMD 120
Qy 121 QAIMDKNIILKANFSVIPERLETLILLRAFTTEGAVGEISPLPSLPGHTNEDVKNAGIV 180
Db 121 QAIMDKNIILKANFSVIPDRLETLILLRAFTTEGAVGEISPLPSLPGHTNEDVKNAGIV 180
Qy 181 LIGGLKWNNDTVRISETLQRFAPWRSSHENGSRPSPPKOKRMERTIEPEV 230
Db 181 LIGGLEWNNNTVRVSKTLQRFAPWRSSNENGRPPLTPKOKRMARTIRSEV 230

RESULT 10
US-10-065-133A-55
; Sequence 55, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 97
; ORGANISM: Equine influenza virus H3N8
US-10-734-373-55

Query Match 41.4%; Score 488; DB 4; Length 97;
Best Local Similarity 99.0%; Pred. No. 1.7e-43;
Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 134 FSVIFERLETLILLRAFTTEGAVGEISPLPSLPGHTNEDVKNAGIVLIGLKNWNTVR 193
Db 1 FSVIFERLETLILLRAFTTEGAVGEISPLPSLPGHTNEDVKNAGIVLIGLKNWNTVR 60
Qy 194 ISETLQRFAPWRSSHENGSRPSPPKOKRMERTIEPEV 230
Db 61 ISETLQRFAPWRSSHENGSRPSPPKOKRMERTIEPEV 97

RESULT 11
US-10-734-373-55
; Sequence 55, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 97
; ORGANISM: Equine influenza virus H3N8
US-10-734-373-55

Query Match 41.4%; Score 488; DB 4; Length 97;
Best Local Similarity 99.0%; Pred. No. 1.7e-43;
Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 134 FSVIFERLETLILLRAFTTEGAVGEISPLPSLPGHTNEDVKNAGIVLIGLKNWNTVR 193
Db 1 FSVIFERLETLILLRAFTTEGAVGEISPLPSLPGHTNEDVKNAGIVLIGLKNWNTVR 60
Qy 194 ISETLQRFAPWRSSHENGSRPSPPKOKRMERTIEPEV 230
Db 61 ISETLQRFAPWRSSHENGSRPSPPKOKRMERTIEPEV 97

RESULT 12
US-10-181-585B-37
; Sequence 37, Application US/10181585B
; Publication No. US20050175985A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System
; APPLICANT: of Higher Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C3-PUS
; CURRENT APPLICATION NUMBER: US/10/181,585B
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: PCT/US01/05048
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/506,286
; PRIOR FILING DATE: 2000-02-16
```

```

; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 37
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-181-585B-37

Query Match      41.4%; Score 488; DB 5; Length 97;
Best Local Similarity 99.0%; Pred. No. 1.7e-43;
Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 134 FSVIFERLETLILLRAFTGEGAVGEISPLPSLPFGHTNEDVKNAGVILGGLKWNNTVR 193
Db 1 FSVIFERLETLILLRAFTGEGAVGEISPLPSLPFGHTNEDVKNAGVILGGLKWNNTVR 60

QY 194 ISETLQFARSSHENGSRPSPKPKKXWERTIEPV 230
Db 61 ISETLQFARSSHENGSRPSPKPKKXWERTIEPV 97

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RESULT 13
US-09-822-827-973
; Sequence 973, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 973
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-822-827-973

Query Match      34.0%; Score 400; DB 3; Length 344;
Best Local Similarity 73.5%; Pred. No. 2.2e-33;
Matches 86; Conservative 8; Mismatches 15; Indels 8; Gaps 2;

QY 1 MDSNTVSSFOVDCFLMHWKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDPNTVSSFOVDCFLMHWKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDLETATRA 60

QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTD-----MTLDEMSEDFWMLMPKQKVT 112
Db 61 GKQIVERILKEESDEALKMTIASVPASRYLTD-----EEFLTPKKLQCVDLHVISNDVCAQVHPQKVT 114

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RESULT 14
US-09-895-793-973
; Sequence 973, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Rasir A.W.
; APPLICANT: Hepler, William T.

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; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895.793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 973
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-793-973

Query Match      34.0%; Score 400; DB 3; Length 344;
Best Local Similarity 73.5%; Pred. No. 2.2e-33;
Matches 86; Conservative 8; Mismatches 15; Indels 8; Gaps 2;

QY 1 MDSNTVSSFOVDCFLMHWKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDPNTVSSFOVDCFLMHWKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDLETATRA 60

QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTD-----MTLDEMSEDFWMLMPKQKVT 112
Db 61 GKQIVERILKEESDEALKMTIASVPASRYLTD-----EEFLTPKKLQCVDLHVISNDVCAQVHPQKVT 114

RESULT 15
US-10-312-089-1
; Sequence 1, Application US/10312089
; Publication No. US20030143240A1
; GENERAL INFORMATION:
; APPLICANT: Cabezon-Silva, Teresa Elisa Virginia
; APPLICANT: Bernanne, Philippe Jean Gervais Ghislain
; TITLE OF INVENTION: Prostate Protein Vaccine Comprising
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: PCT/EP01/07082
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: GB 0015722.2
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-312-089-1

Query Match      32.9%; Score 387; DB 4; Length 312;
Best Local Similarity 44.2%; Pred. No. 4.6e-32;
Matches 96; Conservative 24; Mismatches 55; Indels 42; Gaps 5;

QY 1 MDSNTVSSFOVDCFLMHWKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDPNTVSSFOVDCFLMHWKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDLETATRA 60

QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDEMSEDFWMLMPKQKVT 106
Db 61 GKQIVERILKEESDEALKMTIASVPASRYLTDMTLDEMSEDFWMLMPKQKVT 111

QY 107 PKQKVTGSLCTRMQDAI-----MDK-----NIIKANFSV-----IFERLETLILL 147
Db 112 POWLSAAACFQNSYTTIGLGLHSLDQEPGQWQASLSVRHPEYRNRELLANDMLIKL 171

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Wed Mar 8 09:11:19 2006

Qy 148 RAFTBEGAVVGEISPLSPFGHTNEDVKNAIGVLIIG 184  
Db 172 DESVSESDTIRISIASQCPAGNSCLVSGWGLLANG 208

Search completed: March 7, 2006, 19:25:33  
Job time : 167 secs

GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2006, 19:21:19 ; Search time 47 seconds  
 (without alignments)  
 404,583 Million cell updates/sec

Title: US-10-734-373-58  
 Perfect score: 1178  
 Sequence: 1 MDSNTVSSFQVDCFLMHRK.....RPSFPKQKRMERTIEPV 230

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database :

Issued Patents AA.\*  
 1: /cgn2\_6/ptodata/1/iaa/5 COMB.pap.\*  
 2: /cgn2\_6/ptodata/1/iaa/6 COMB.pap.\*  
 3: /cgn2\_6/ptodata/1/iaa/H COMB.pap.\*  
 4: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pap.\*  
 5: /cgn2\_6/ptodata/1/iaa/RE COMB.pap.\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1178	100.0	230	2	US-09-506-286B-51
2	1178	100.0	230	2	US-09-506-286B-58
3	1178	100.0	230	2	US-10-065-133A-51
4	1178	100.0	230	2	US-10-065-133A-58
5	1010	85.7	237	1	US-08-467-587A-4
6	488	41.4	97	2	US-09-506-286B-55
7	488	41.4	97	2	US-10-065-133A-55
8	392.5	33.3	306	4	PCT-US94-01149-10
9	390.5	33.1	337	1	US-08-441-857-8
10	390.5	33.1	337	2	US-08-193-159-8
11	390.5	33.1	337	2	US-09-283-646C-8
12	389.5	33.1	230	4	PCT-US94-01149-12
13	389.5	33.1	230	4	PCT-US94-01149-72
14	389.5	33.1	304	4	PCT-US94-01149-55
15	389.5	33.1	304	4	PCT-US94-01149-57
16	387.5	32.9	225	4	PCT-US94-01149-30
17	387.5	32.9	231	4	PCT-US94-01149-29
18	387.5	32.9	242	4	PCT-US94-01149-18
19	385.5	32.7	150	1	US-08-388-267C-4
20	385.5	32.7	150	2	US-09-277-720-4
21	385.5	32.7	338	1	US-08-441-857-12
22	385.5	32.7	338	2	US-08-193-159-12
23	385.5	32.7	338	2	US-09-283-646C-12
24	385	32.7	226	4	PCT-US94-01149-26
25	384	32.6	168	4	PCT-US94-01149-27
26	384	32.6	163	4	PCT-US94-01149-28
27	384	32.6	238	4	PCT-US94-01149-24

28	384	32.6	304	4	PCT-US94-01149-32	Sequence 32, Appl
29	384	32.6	307	4	PCT-US94-01149-16	Sequence 16, Appl
30	380	32.3	338	1	US-08-441-857-10	Sequence 10, Appl
31	380	32.3	338	2	US-08-193-159-10	Sequence 10, Appl
32	380	32.3	338	2	US-09-283-646C-10	Sequence 10, Appl
33	377.5	32.0	339	1	US-08-441-857-6	Sequence 6, Appl
34	377.5	32.0	339	2	US-08-193-159-6	Sequence 6, Appl
35	377.5	32.0	339	2	US-09-283-646C-6	Sequence 6, Appl
36	222	18.8	209	4	PCT-US94-01149-14	Sequence 14, Appl
37	215.5	18.3	209	4	PCT-US94-01149-22	Sequence 22, Appl
38	214	18.2	269	4	PCT-US94-01149-20	Sequence 20, Appl
39	89.5	7.6	1876	2	US-09-418-710-71	Sequence 71, Appl
40	89.5	7.6	1876	2	US-09-839-479-70	Sequence 70, Appl
41	87.5	7.4	844	2	US-09-813-148-4	Sequence 4, Appl
42	87.5	7.4	844	2	US-09-590-304-4	Sequence 4, Appl
43	87.5	7.4	844	2	US-09-432-361-34	Sequence 34, Appl
44	87.5	7.4	844	2	US-09-866-020A-29	Sequence 29, Appl
45	87.5	7.4	872	2	US-09-177-650-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
 US-09-506-286B-51  
 ; Sequence 51, Application US/09506286B  
 ; Patent No. 6482414  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dowling, Patricia W.  
 ; APPLICANT: Youngner, Julius S.  
 ; APPLICANT: The University of Pittsburgh, of the Commonwealth  
 ; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
 ; FILE REFERENCE: EQ-1-C2  
 ; CURRENT APPLICATION NUMBER: US/09/506,286B  
 ; PRIOR FILING DATE: 2000-02-16  
 ; PRIOR FILING DATE: 1998-08-13  
 ; PRIOR APPLICATION NUMBER: PCT/US99/18583  
 ; PRIOR FILING DATE: 1999-08-12  
 ; NUMBER OF SEQ ID NOS: 108  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 51  
 ; LENGTH: 230  
 ; TYPE: PRT  
 ; ORGANISM: Equine influenza virus H3N8  
 US-09-506-286B-51

Query Match 100.0%; Score 1178; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-124;  
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDSNTVSSFQVDCFLMHRKRRFADQELGDAPFLDLRRDQKSLKRGSTGLGDIETATRA	60
DB	1	MDSNTVSSFQVDCFLMHRKRRFADQELGDAPFLDLRRDQKSLKRGSTGLGDIETATRA	60
QY	61	GRQIVEQLLEESDEALKMTIASVPASRYLTDMTLDEMSPMLMPKQKVTGSLCIRMD	120
DB	61	GRQIVEQLLEESDEALKMTIASVPASRYLTDMTLDEMSPMLMPKQKVTGSLCIRMD	120
QY	121	QAIMDKNIILKANFSVIFERLETLILLRAFTGAGVGEISPLSPGHTNEDVKNAGV	180
DB	121	QAIMDKNIILKANFSVIFERLETLILLRAFTGAGVGEISPLSPGHTNEDVKNAGV	180
QY	181	LIGGLKWNNTVRISETLQFAWRSHSHGRRSPFPKQKEMRTIEPV	230
DB	181	LIGGLKWNNTVRISETLQFAWRSHSHGRRSPFPKQKEMRTIEPV	230

RESULT 2  
 US-09-506-286B-58  
 ; Sequence 58, Application US/09506286B  
 ; Patent No. 6482414  
 ; GENERAL INFORMATION:

```
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 58
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-58

Query Match      100.0%; Score 1178; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 2.1e-124; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 0;

Qy 1 MDSNTVSSFOVDCFLMHWVRKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDSNTVSSFOVDCFLMHWVRKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Qy 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNDTVRISETLQRFARWSSHENGSRPSFPKQKRWERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLQRFARWSSHENGSRPSFPKQKRWERTIEPEV 230
Qy 181 LIGGLKWNNDTVRISETLQRFARWSSHENGSRPSFPKQKRWERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLQRFARWSSHENGSRPSFPKQKRWERTIEPEV 230

RESULT 3
US-10-065-133A-51
; Sequence 51, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR FILING DATE: 1999-08-12
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 51
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-51

Query Match      100.0%; Score 1178; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 2.1e-124; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 0;

Qy 1 MDSNTVSSFOVDCFLMHWVRKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDSNTVSSFOVDCFLMHWVRKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Qy 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNDTVRISETLQRFARWSSHENGSRPSFPKQKRWERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLQRFARWSSHENGSRPSFPKQKRWERTIEPEV 230

RESULT 4
US-10-065-133A-58
; Sequence 58, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR FILING DATE: 1999-08-12
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 58
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-58

Query Match      100.0%; Score 1178; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 2.1e-124; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 0;

Qy 1 MDSNTVSSFOVDCFLMHWVRKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDSNTVSSFOVDCFLMHWVRKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Qy 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNDTVRISETLQRFARWSSHENGSRPSFPKQKRWERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLQRFARWSSHENGSRPSFPKQKRWERTIEPEV 230

RESULT 5
US-08-467-587A-4
; Sequence 4, Application US/08467587A
; Patent No. 5843724
; GENERAL INFORMATION:
; APPLICANT: KRUG, ROBERT M.
; APPLICANT: QIAN, XIAO YAN
; TITLE OF INVENTION: CHIMERIC NUCLEIC ACIDS AND PROTEINS
; TITLE OF INVENTION: FOR INHIBITING HIV-1 EXPRESSION
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Steinberg, Raskin & Davidson, P.C.
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
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Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNDTVRISETLQRFARWSSHENGSRPSFPKQKRWERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLQRFARWSSHENGSRPSFPKQKRWERTIEPEV 230

RESULT 4
US-10-065-133A-58
; Sequence 58, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR FILING DATE: 1999-08-12
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 58
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-58

Query Match      100.0%; Score 1178; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 2.1e-124;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLMHWVRKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDSNTVSSFOVDCFLMHWVRKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Qy 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNDTVRISETLQRFARWSSHENGSRPSFPKQKRWERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLQRFARWSSHENGSRPSFPKQKRWERTIEPEV 230

RESULT 5
US-08-467-587A-4
; Sequence 4, Application US/08467587A
; Patent No. 5843724
; GENERAL INFORMATION:
; APPLICANT: KRUG, ROBERT M.
; APPLICANT: QIAN, XIAO YAN
; TITLE OF INVENTION: CHIMERIC NUCLEIC ACIDS AND PROTEINS
; TITLE OF INVENTION: FOR INHIBITING HIV-1 EXPRESSION
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Steinberg, Raskin & Davidson, P.C.
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
```



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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,587A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/429,761
; FILING DATE: 27-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Davidson, Clifford M.
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 614.1001CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-768-3800
; TELEFAX: (212)-382124
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: LINEAR
;
US-08-467-587A-4
Query Match 85.7%; Score 1010; DB 1; Length 237;
Best Local Similarity 83.9%; Pred. No. 1.9e-105;
Matches 193; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 1 MDSNTVSSFDVCFMHVRKRFADQELGDPFLDRLRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFDVCFMHVRKQVVDQELGDPFLDRLRDQKSLKGRGSLGLNIEAATHV 60

QY 61 GQIQVEQILEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GQIQVEKILKEESDEALKMTASTPASRYITDWTIELSRDWFMLMPKQKVEGPLCIRID 120

QY 121 QAIMDKNIIKANSVIFERLETLILLRAFTGAGVGEISPLPSLPQHTNEDVKNAIGV 180
DB 121 QAIMDKNIIKANSVIFDELETLILLRAFTGAGVGEISPLPSLPFGHTIEDVKNAIGV 180

QY 181 LIGGLEKNDNTVRSETLORFAWRSSHENGSRPSPKQKRMERTIEPV 230
DB 181 LIGGLEKNDNTVRSKTLQRFAGWSSNENGRPPLTPKQKRMARTARSKV 230

RESULT 6
US-09-506-286B-55
; Sequence 55, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 55
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-55
Query Match 41.4%; Score 488; DB 2; Length 97;
Best Local Similarity 93.0%; Pred. No. 3.5e-47;
Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 134 FSVIFERLETLILLRAFTGAGVGEISPLPSLPQHTNEDVKNAIGVILGGLKNDNTVR 193
DB 1 FSVIFERLETLILLRAFTGAGVGEISPLPSLPQHTNEDVKNAIGVILGGLKNDNTVR 60

QY 194 ISETLORFAWRSSHENGSRPSPKQKRMERTIEPV 230
DB 61 ISETLORFAWRSSHENGSRPSPKQKRMERTIEPV 97

RESULT 7
US-10-065-133A-55
; Sequence 55, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 09/133,921
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 55
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-55
Query Match 41.4%; Score 488; DB 2; Length 97;
Best Local Similarity 99.0%; Pred. No. 3.5e-47;
Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 134 FSVIFERLETLILLRAFTGAGVGEISPLPSLPQHTNEDVKNAIGVILGGLKNDNTVR 193
DB 1 FSVIFERLETLILLRAFTGAGVGEISPLPSLPQHTNEDVKNAIGVILGGLKNDNTVR 60

QY 194 ISETLORFAWRSSHENGSRPSPKQKRMERTIEPV 230
DB 61 ISETLORFAWRSSHENGSRPSPKQKRMERTIEPV 97

RESULT 8
PCT-US94-01149-10
; Sequence 10, Application PC/TUS9401149
; GENERAL INFORMATION:
; APPLICANT: Shatzman, Allan
; APPLICANT: Scott, Miller
; APPLICANT: Dillon, Susan B.
; APPLICANT: Kane, James
; TITLE OF INVENTION: Vaccinal Polypeptides
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; ADDRESS: Patents
; STREET: U.S. Mailcode UW2220 - 709 Swedeland Road
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01149
; FILING DATE:
; CLASSIFICATION:

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Wed Mar 8 09:11:19 2006

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 149,150
; FILING DATE: 05-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 013,415
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 108,914
; FILING DATE: 18-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 837,773
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 751,896
; FILING DATE: 30-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 387,200
; FILING DATE: 28-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 238,801
; FILING DATE: 02-NOV-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 645,732
; FILING DATE: 30-AUG-1984
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50134 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-270-5096
; TELEFAX: 215-270-5090
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 306 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-01149-10

Query Match 33.3%; Score 392.5; DB 4; Length 306;
Best Local Similarity 47.8%; Pred. No. 1.2e-35;
Matches 100; Conservative 28; Mismatches 56; Indels 23; Gaps 8;

QY 1 MDSNTVSSFOVDCFLWHVVKRFADQELGDAPFLDRLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDPNTVSSFOVDCFLWHVVKRFADQELGDAPFLDRLRRDQKSLKGRGSLGLDLETATRA 60
QY 61 GKQIVEQLLEESDEALKMTIASVPSRYLTDMTDEMSE-----DWFMKPKQKVTGSL 115
Db 61 GKQIVERILKEESDEALKMTGKQNV-----SLDEKNSVSVDPGKMKVLSKKNKD 120
QY 116 C-IRMDQAINDK-----NIIKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLP 168
Db 121 ADLSTQAIDQINGKLNRIEKTNEK--FHQIE-----KEFSE---VEGRIQDLEKYVE 170
QY 169 HTNEDVKNAIGVLIGLKWNTVRISET 197
Db 171 DTKIDLWSYNALLVALE-NQHTIDLDS 198

RESULT 9
US-08-441-857-8
; Sequence 8, Application US/08441857
; Patent No. 594236
; GENERAL INFORMATION:
; APPLICANT: SIMON, MARKUS
; APPLICANT: KRAMER, MICHAEL
; APPLICANT: SCHAIBLE, ULRICH
; APPLICANT: WALLICH, REINHARD
; APPLICANT: LOBET, YVES
; TITLE OF INVENTION: OSP A PROTEINS OF BORRELIA BURGDORFERI SUBGROUPS, ENCODING GE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

```

```

;
; ADDRESSEE: SMITHKLINE BEECHAM CORPORATION/CORPORATE INTELLECTUAL PROPERTY-UW
; STREET: P.O. BOX 1539
; CITY: KING OF PRUSSIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,857
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/193,159
; FILING DATE: JULY 5, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JEFFREY A. SUTTON
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: B45008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270 5024
; TELEFAX: (610) 270 5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: BORRELIA BURGDORFERI
; STRAIN: 19857
; IMMEDIATE SOURCE:
; CLONE: NSI-19857
; US-08-441-857-8

Query Match 33.1%; Score 390.5; DB 1; Length 337;
Best Local Similarity 42.4%; Pred. No. 2.3e-35;
Matches 112; Conservative 21; Mismatches 58; Indels 73; Gaps 10;

QY 1 MDSNTVSSFOVDCFLWHVVKRFADQELGDAPFLDRLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDPNTVSSFOVDCFLWHVVKRFADQELGDAPFLDRLRRDQKSLKGRGSLGLDLETATRA 60
QY 61 GKQIVEQLLEESDEALKMTIASVPSRYLTDMTDEMSE-----DWFMKPKQKVTG 113
Db 61 GKQIVERILKEESDEALKMTGKQNV-----SLDEKNSVSVDPGKMKVLSKKNKD 114
QY 114 SLICRMDQAINDKNIIILKA-----NFSVIFERLE-----TLILLRAFTTEG 154
Db 115 G---KYDILMATVDNVDLKGTSKNGSGILEGVKADKSKVKLTVADDLSKTTLEVLKEDG 171
QY 155 AVV-----GEISPLPSLPGH-----TNED-VKNAIGVLIGGL 185
Db 172 TVVSRKVTSKDKSTTEAKFNKSGELSEKMTFRANGTTLEYSQMTNEDNAKAVETLNKI 231
QY 186 KWNDN-----TVRISE---TLQR 200
Db 232 KPEGNLASGKTAVEIKEGTIVLKR 255

RESULT 10
US-08-193-159-8
; Sequence 8, Application US/08193159
; Patent No. 6113914
; GENERAL INFORMATION:
; APPLICANT: SIMON, MARKUS
; APPLICANT: KRAMER, MICHAEL
; APPLICANT: SCHAIBLE, ULRICH

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; APPLICANT: WALLICH, REINHARD
; APPLICANT: LOBET, YVES
; TITLE OF INVENTION: OSP A PROTEINS OF BORRELIA BURGDORFERI SUBGROUPS, ENCODING GE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SMITHKLINE BEECHAM CORPORATION/CORPORATE INTELLECTUAL PROPERTY-UW
; STREET: P.O. BOX 1539
; CITY: KING OF PRUSSIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,159
; FILING DATE: JULY 5, 1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: JEFFREY A. SUTTON
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: B45008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270 5024
; TELEFAX: (610) 270 5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: BORRELIA BURGDORFERI
; STRAIN: 19857
; IMMEDIATE SOURCE:
; CLONE: NS1-19857
; US-08-193-159-8

Query Match 33.1%; Score 390.5; DB 2; Length 337;
Best Local Similarity 42.4%; Pred. No. 2.3e-35;
Matches 112; Conservative 21; Mismatches 58; Indels 73; Gaps 10;

QY 1 MDSNTVSSFQVDCFLMHWKRFADQELGDPFLDRLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDPNTVSSFQVDSFLMHWKRVADQELGDPFLDRLRRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVQEILKEESDEALKMTIASVPASRYLTDWLTDEMSR-----DWFMLMPKQKVTG 113
DB 61 GKQIVQEILKEESDEALKMTGKQNV-----SLDEKNSVSDVPGMKVLVSKEKND 114
QY 114 SLICRMDQAIMDKNIILKA-----NFSVIFERLE-----TLILRAFTREG 154
DB 115 G----KYDLMATVNDVLDKGTSDKNNGSGILEGVKADKSKVLTAVADDLSKTTLEVLKEDG 171
QY 155 AVV-----GEISPLPSLPGH-----TNE-D-VKNAIGVLIGGL 185
DB 172 TVSVRKVTSKDKSTTEAKFNKSGELSEKTMTRANGTTLEYSQMTNEDNAKAVETLKNGI 231
QY 186 KWNND-----TVRISE---TLQR 200
DB 232 KFEGLASGKTAVEIKEGTVTLKR 255

RESULT 11
US-09-283-646C-8
; Sequence 8, Application US/09283646C
; Patent No. 6676942
; GENERAL INFORMATION:
; APPLICANT: Simon, Markus

```

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; APPLICANT: Kramer, Michael
; APPLICANT: Schaible, Ulrich
; APPLICANT: Wallich, Reinhard
; APPLICANT: Lobet, Yves
; TITLE OF INVENTION: OSP A PROTEINS OF BORRELIA BURGDORFERI
; FILE REFERENCE: B45008-C1-C1
; CURRENT APPLICATION NUMBER: US/09/283,646C
; CURRENT FILING DATE: 1999-04-01
; PRIOR FILING DATE: 1995-05-16
; PRIOR APPLICATION NUMBER: 08/441,857
; PRIOR FILING DATE: 1994-07-05
; PRIOR APPLICATION NUMBER: PCT/EP92/01827
; PRIOR FILING DATE: 1992-08-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PASTSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 337
; TYPE: PRT
; ORGANISM: BORRELIA BURGDORFERI
; US-09-283-646C-8

Query Match 33.1%; Score 390.5; DB 2; Length 337;
Best Local Similarity 42.4%; Pred. No. 2.3e-35;
Matches 112; Conservative 21; Mismatches 58; Indels 73; Gaps 10;

QY 1 MDSNTVSSFQVDCFLMHWKRFADQELGDPFLDRLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDPNTVSSFQVDSFLMHWKRVADQELGDPFLDRLRRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVQEILKEESDEALKMTIASVPASRYLTDWLTDEMSR-----DWFMLMPKQKVTG 113
DB 61 GKQIVQEILKEESDEALKMTGKQNV-----SLDEKNSVSDVPGMKVLVSKEKND 114
QY 114 SLICRMDQAIMDKNIILKA-----NFSVIFERLE-----TLILRAFTREG 154
DB 115 G----KYDLMATVNDVLDKGTSDKNNGSGILEGVKADKSKVLTAVADDLSKTTLEVLKEDG 171
QY 155 AVV-----GEISPLPSLPGH-----TNE-D-VKNAIGVLIGGL 185
DB 172 TVSVRKVTSKDKSTTEAKFNKSGELSEKTMTRANGTTLEYSQMTNEDNAKAVETLKNGI 231
QY 186 KWNND-----TVRISE---TLQR 200
DB 232 KFEGLASGKTAVEIKEGTVTLKR 255

RESULT 12
PCT-US94-01149-12
; Sequence 12, Application PC/TUS9401149
; GENERAL INFORMATION:
; APPLICANT: Shatzman, Allan
; APPLICANT: Scott, Miller
; APPLICANT: Dillon, Susan B.
; APPLICANT: Kane, James
; TITLE OF INVENTION: Vaccinal Polypeptides
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; ADDRESSEE: Patents
; STREET: U.S. Mailcode UW2220 - 709 Swedeland Road
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01149

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;
; FILING DATE:
; CLASSIFICATION:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01149
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 149,150
; FILING DATE: 05-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 013,415
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 108,914
; FILING DATE: 18-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 837,773
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 751,896
; FILING DATE: 30-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 387,200
; FILING DATE: 28-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 238,801
; FILING DATE: 02-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 645,732
; FILING DATE: 30-AUG-1984
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50134 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-270-5096
; TELEFAX: 215-270-5090
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-01149-12

Query Match 33.1%; Score 389.5; DB 4; Length 230;
Best Local Similarity 78.8%; Pred. No. 1.7e-35;
Matches 78; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

Qy 1 MDSNTVSSFQVDCFLMHWKRFADQELGDAPFLDLRRDQKSLKRGSTGLGDIETATRA 60
Db 1 MDPNTVSSFQVDCFLMHWKRVADQELGDAPFLDLRRDQKSLKRGSTGLGDIETATRA 60
Qy 61 GKQIVEQLLEESDEALKMTIASV---PASRYLTDMTLD 96
Db 61 GKQIVERILKEESDEALKMTDMLIQDLEKYVEDTKID 99

RESULT 13
PCT-US94-01149-72
; Sequence 72, Application PC/TUS9401149
; GENERAL INFORMATION:
; APPLICANT: Shatzman, Allan
; APPLICANT: Scott, Miller
; APPLICANT: Dillon, Susan B.
; APPLICANT: Kane, James
; TITLE OF INVENTION: Vaccinal Polypeptides
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; STREET: U.S. Mailcode UW2220 - 709 Swedeland Road
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:

Query Match 33.1%; Score 389.5; DB 4; Length 230;
Best Local Similarity 78.8%; Pred. No. 1.7e-35;
Matches 78; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

Qy 1 MDSNTVSSFQVDCFLMHWKRFADQELGDAPFLDLRRDQKSLKRGSTGLGDIETATRA 60
Db 1 MDPNTVSSFQVDCFLMHWKRVADQELGDAPFLDLRRDQKSLKRGSTGLGDIETATRA 60
Qy 61 GKQIVEQLLEESDEALKMTIASV---PASRYLTDMTLD 96
Db 61 GKQIVERILKEESDEALKMTDMLIQDLEKYVEDTKID 99

RESULT 14
PCT-US94-01149-55
; Sequence 55, Application PC/TUS9401149
; GENERAL INFORMATION:
; APPLICANT: Shatzman, Allan
; APPLICANT: Scott, Miller
; APPLICANT: Dillon, Susan B.
; APPLICANT: Kane, James
; TITLE OF INVENTION: Vaccinal Polypeptides
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; STREET: U.S. Mailcode UW2220 - 709 Swedeland Road
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
```

STREET: U.S. Mailcode UW2220 - 709 Swedeland Road  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-2799

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01149  
FILING DATE: 01-FEB-1993

CLASSIFICATION:  
PCT/US94/01149

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 149,150  
FILING DATE: 05-NOV-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 013,415  
FILING DATE: 01-FEB-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 108,914  
FILING DATE: 18-AUG-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 837,773  
FILING DATE: 18-FEB-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 751,896  
FILING DATE: 30-AUG-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 387,200  
FILING DATE: 28-JUL-1989  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 238,801  
FILING DATE: 02-NOV-1988  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 645,732  
FILING DATE: 30-AUG-1984  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50134 PCT  
TELEPHONE: 215-270-5096  
TELEFAX: 215-270-5090  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 304 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-01149-55

Query Match 33.1%; Score 389.5; DB 4; Length 304;  
Best Local Similarity 37.9%; Pred. No. 2.5e-35;  
Matches 99; Conservative 36; Mismatches 47; Indels 79; Gaps 7;  
Qy 1 MDSNTVSSQVDFLHVHVRKRFADQELGDPFLDLRLRDQKSLKGRGSLGLDIETATRA 60  
Db 1 MDPNTVSSQVDFLHVHVRKRVADQELGDPFLDLRLRDQKSLKGRGSLGLDIETATRA 60  
Qy 61 GKQIIVEQLLEESDEALKMTI-----ASVPASRY 89  
Db 61 GKQIIVERILKEESDEALKMTGFGAAGLEGCGWEGHGYTSHCAHGAVAADLK 120  
Qy 90 LTDMTLDMSRDWFLMP-----KQKVTGSL-----CIRMDQAINDKNIIILKANESVIP 138  
Db 121 STQEAINKITKNLYLSELVKNLQELSGANNLHDEILDEKVD-----LRAD--TIS 174  
Qy 139 ERLETLILIRAFTEGAVGCEISPLPFGHTNEDVKNALGVILGLKNDNTVRISETL 198  
Db 175 SQELAVILL---SNEGIISE-----DEHLALERKL 203

Qy 199 ORFAWRSSHENGRSPFPKQK 219  
Db 204 KKMGLGPSAVEIGNGCFETKHK 224  
RESULT 15  
PCT-US94-01149-57  
GENERAL INFORMATION:  
SEQUENCE 57, Application PC/TUS9401149  
APPLICANT: Shatzman, Allan  
APPLICANT: Scott, Miller  
APPLICANT: Dillo, Susan B.  
APPLICANT: Kane, James  
TITLE OF INVENTION: Vaccinal Polypeptides  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Smithline Beecham Corporation - Corporate  
ADDRESSEE: Patents  
STREET: U.S. Mailcode UW2220 - 709 Swedeland Road  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01149  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 149,150  
FILING DATE: 05-NOV-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 013,415  
FILING DATE: 01-FEB-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 108,914  
FILING DATE: 18-AUG-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 837,773  
FILING DATE: 18-FEB-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 751,896  
FILING DATE: 30-AUG-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 387,200  
FILING DATE: 28-JUL-1989  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 238,801  
FILING DATE: 02-NOV-1988  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 645,732  
FILING DATE: 30-AUG-1984  
ATTORNEY/AGENT INFORMATION:  
NAME: Baumeister, Kirk  
REGISTRATION NUMBER: 33,833  
REFERENCE/DOCKET NUMBER: P50134 PCT  
TELEPHONE: 215-270-5096  
TELEFAX: 215-270-5090  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 304 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-01149-57

Query Match 33.1%; Score 389.5; DB 4; Length 304;  
Best Local Similarity 37.9%; Pred. No. 2.5e-35;

Matches		99; Conservative	36; Mismatches	47; Indels	79; Gaps	7;
Qy	1	MDSNTVSSFQVDCFLHVRKRPADQELGDAPFLDRLRRDOKSLKRGSTGLGDIETATRA	60			
Db	1	MDPNTVSSFQVDCFLHVRKRVADQELGDAPFLDRLRRDOKSLKRGSTGLGDIETATRA	60			
Qy	61	GKQIVEQILEESDEALKMTI-----ASVPASRY	89			
Db	61	GKQIVERILKEESDEALKMTI-----ASVPASRY	89			
Qy	90	LTDMTLDEMSRDWFLMP-----KQKVTGSL-----CIRMDQAIMDKNIILKANFSVIF	138			
Db	121	STQEAINKITKNLNYLSELEVKNLQRLSGAMNELHDEILELDEKVDV-----LRAD--TIS	174			
Qy	139	ERLETILILIRAFTEEGAVVGEISPLSPFGHTNEDVKNAIGVLIGLKNWNTVRISETL	198			
Db	175	SOILELAVLL---SNEGIINSE-----DEHLALERKL	203			
Qy	199	QRFARWSSHENGSRPSPPKOK	219			
Db	204	KKMLGFSAVEIGNGCFETGKH	224			

Search completed: March 7, 2006, 19:22:42  
Job time : 49 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run On: March 7, 2006, 19:17:24 ; Search time 40 Seconds  
(without alignment)  
553.246 Million cell updates/sec

Title: US-10-734-373-58  
Perfect score: 1178  
Sequence: 1 MDSNTVSSQVDCFLMHRK.....RPSPPKQKRMERTIEPEV 230

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1110	94.2	230	1 MNIVA2	nonstructural prot
2	1097	93.1	230	1 MNIVA3	nonstructural prot
3	1093	92.8	230	1 MNIVA4	nonstructural prot
4	1083	91.9	227	1 MNIVX9	nonstructural prot
5	1075	91.3	230	1 MNIV1F	nonstructural prot
6	1074	91.2	227	1 MNIVX3	nonstructural prot
7	1073	91.1	230	1 MNIV1A	nonstructural prot
8	1066	90.5	227	1 MNIVX5	nonstructural prot
9	1055	89.6	227	1 MNIVC1	nonstructural prot
10	1054	89.5	227	1 MNIVX7	nonstructural prot
11	1053	89.4	237	1 MNIV14	nonstructural prot
12	1052	89.3	230	1 MNIV17	nonstructural prot
13	1051	89.2	227	1 MNIV1	nonstructural prot
14	1051	89.2	227	1 MNIVX1	nonstructural prot
15	1048	89.0	230	2 S09648	nonstructural prot
16	1041	88.4	230	1 D45539	nonstructural prot
17	1010	85.7	237	1 MNIV61	nonstructural prot
18	1007	85.5	217	1 MNIV61	nonstructural prot
19	995	84.5	237	1 MNIV1K	nonstructural prot
20	949	80.6	202	1 MNIV47	nonstructural prot
21	852	72.3	230	1 MNIV16	nonstructural prot
22	848	72.0	230	1 MNIVA5	nonstructural prot
23	848	72.0	230	1 MNIVA6	nonstructural prot
24	846	71.8	230	1 MNIVA8	nonstructural prot
25	845	71.7	230	1 MNIV17	nonstructural prot
26	833	70.7	230	2 A45575	nonstructural prot
27	429	36.4	124	1 MNIV11	nonstructural prot
28	406	34.5	89	2 B92982	nonstructural prot
29	149	12.6	32	2 PQ0419	nonstructural prot

30	135	11.5	32	2 PQ0425	nonstructural prot
31	133	11.3	32	2 PQ0413	nonstructural prot
32	93	7.9	189	2 C87606	RNA polymerase sig
33	93	7.9	245	2 A97073	transcription regu
34	89	7.6	421	2 AD2305	gamma-glutamyl rho
35	89	7.6	1448	2 P83237	probable ATP-depen
36	88.5	7.5	718	2 T05840	subtilisin-like pr
37	85.5	7.3	291	2 H70878	hypothetical prote
38	85.5	7.3	432	2 T10894	neutrophil pentraxin
39	85	7.2	436	2 P86486	protein F8J9.3 li
40	85	7.2	523	2 S61017	hypothetical prote
41	85	7.2	943	2 F69543	ATP-dependent RNA
42	84	7.1	337	2 AF1630	cell-shape determi
43	83.5	7.1	185	2 S54088	hypothetical prote
44	83.5	7.1	871	2 D86355	protein T16E15.12
45	83	7.0	421	2 B97106	probable ATPase re

ALIGNMENTS

RESULT 1

MNIVA2  
nonstructural protein NS1 - influenza A virus (strain A/mallard/New York/6750/78)  
C:Species: influenza A virus  
C>Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
C:Accession: C32662  
R:Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.  
A>Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, Virolgy 171, 1-9, 1989  
A:Reference number: A32662; MUID:89299445; PMID:2525836  
A:Accession: C32662  
A:Molecule type: genomic RNA  
A:Residues: 1-230 <TRE>  
A:Cross-references: UNIPROT:P13138; UNIPARC:UPI0000174ABA  
C:Genetics:  
A:Gene: NS1  
A:Map position: segment 8  
C:Superfamily: influenza virus nonstructural protein NS1  
C:Keywords: alternative splicing; nonstructural protein

Query Match 94.2%; Score 1110; DB 1; Length 230;  
Best Local Similarity 93.5%; Pred. No. 3.2e-87;  
Matches 215; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy	1	MDSNTVSSQVDCFLMHRKGFADQELGDAPFLDLRLDQKSLKGRGSLGLDIETATRA	60
Db	1	MDSNTVSSQVDCFLMHRKGFADQELGDAPFLDLRLDQKSLKGRGSLGLDIETATRA	60
Qy	61	GKQIVRQILEEESDEALQWTIASVPASRYLTDMTLDMSRDWFMPLKQKVTGSLCIRMD	120
Db	61	GKQIVRQILEEESDEALQWTIASVPASRYLTDMTLEMSRDWFMPLKQKVTGSLCIRMD	120
Qy	121	QATMDKNITLKANFSVIFERLETLILLRAFTGEGAVCEISPLSPGHTNEDVKNAIGV	180
Db	121	QATMDKNITLKANFSVIFERLETLILLRAFTGEGAVCEISPLSPGHTNEDVKNAIGV	180
Qy	181	LIGGLKWNQTVRISETLQRPWRSSHENGSRFPFPKQKRMERTIEPEV	230
Db	181	LIGGLEWNTVVRSETLQRPWRSSNENGRPPLPKQKRMARTIESEV	230

RESULT 2

MNIVA3  
nonstructural protein NS1 - influenza A virus (strain A/mallard/New York/6974/78)  
C:Species: influenza A virus  
C>Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
C:Accession: B32662  
R:Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.  
A>Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, Virolgy 171, 1-9, 1989  
A:Reference number: A32662; MUID:89299445; PMID:2525836  
A:Accession: B32662

nonstructural protein NS1 - influenza A virus (strain A/Mynah/Haneda-Thai/76 [H3N1]) (fr:  
C:Species: influenza A virus  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 16-Jul-1999  
C:Accession: U0000174AB  
R:Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.  
Virology 158, 465-468, 1987  
A:Title: Genetic divergence of the NS genes of avian influenza viruses.  
A:Reference number: A94361; MUID:87236215; PMID:2954302  
A:Accession: U0000174AB  
A:Molecule type: genomic RNA  
A:Residues: 1-227 <NA>  
A:Cross-references: UNIPARC:UPI0000138A5C; GB:M17070; NID:G324854; PIDN:AAA43548.1; PID:  
C:Genetics: NS1  
A:Map position: segment 8  
C:Superfamily: influenza virus nonstructural protein NS1  
C:Keywords: alternative splicing; nonstructural protein

Query Match 91.9%; Score 1083; DB 1; Length 227;  
Best Local Similarity 92.1%; Pred. No. 6.3e-85;  
Matches 209; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 4 NTSSSFQVDCFLWHVRRKRFADQELGDAPFLDLRRDQSLKGRGSLGLDITATRA 63  
DB 1 NTSSSFQVDCFLWHVRRKRFADQELGDAPFLDLRRDQSLKGRGSLGLDITATRA 60  
QY 64 IVEQILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 123  
DB 61 IVEQILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120  
QY 124 MDKNILKANFSVIFERLETLILLRAFTTEGAIVGEISPLSPGHTNEDVKNAIGV 183  
DB 121 MDKNILKANFSVIFERLETLILLRAFTTEGAIVGEISPLSPGHTNEDVKNAIGV 180  
QY 184 LGGLKNDNTVRISSETLQRFAMRSSHENGSRPFPKQKRMERTIEPEV 230  
DB 181 LGGLKNDNTVRISSETLQRFAMRSSHENGSRPFPKQKRMERTIEPEV 227

RESULT 5  
nonstructural protein NS1 - influenza A virus  
C:Species: influenza A virus  
C:Date: 31-Oct-1980 #sequence\_revision 31-Oct-1980 #text\_change 30-Sep-1993  
C:Accession: A04091  
R:Porter, A.G.; Smith, J.C.; Emtage, J.S.  
Proc. Natl. Acad. Sci. U.S.A. 77, 5074-5078, 1980  
A:Title: Nucleotide sequence of influenza virus RNA segment 8 indicates that coding regi  
A:Reference number: A93858; MUID:81054909; PMID:6254054  
A:Accession: A04091  
A:Molecule type: mRNA  
A:Residues: 1-230 <P>  
A:Cross-references: UNIPARC:UPI0000138A58  
A:Experimental source: strain Rostock  
C:Superfamily: influenza virus nonstructural protein NS1  
C:Keywords: alternative splicing

Query Match 91.3%; Score 1075; DB 1; Length 230;  
Best Local Similarity 89.1%; Pred. No. 3.1e-84;  
Matches 205; Conservative 16; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDSNTVSSSFQVDCFLWHVRRKRFADQELGDAPFLDLRRDQSLKGRGSLGLDITATRA 60  
DB 1 MDSNTVSSSFQVDCFLWHVRRKRFADQELGDAPFLDLRRDQSLKGRGSLGLDITATRA 60  
QY 61 GKOIVQEILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120  
DB 61 GKOIVQEILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120  
QY 121 QAIMDKNIIKANFSVIFERLETLILLRAFTTEGAIVGEISPLSPGHTNEDVKNAIGV 180  
DB 121 QAIMDKNIIKANFSVIFERLETLILLRAFTTEGAIVGEISPLSPGHTNEDVKNAIGV 180

A:Molecule type: genomic RNA  
A:Residues: 1-230 <TRE>  
A:Cross-references: UNIPROT:P13139; UNIPARC:UPI0000174AB  
C:Genetics: NS1  
A:Map position: segment 8  
C:Superfamily: influenza virus nonstructural protein NS1  
C:Keywords: alternative splicing; nonstructural protein

Query Match 93.1%; Score 1097; DB 1; Length 230;  
Best Local Similarity 92.6%; Pred. No. 4.1e-86;  
Matches 213; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDSNTVSSSFQVDCFLWHVRRKRFADQELGDAPFLDLRRDQSLKGRGSLGLDITATRA 60  
DB 1 MDSNTVSSSFQVDCFLWHVRRKRFADQELGDAPFLDLRRDQSLKGRGSLGLDITATRA 60  
QY 61 GKOIVQEILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120  
DB 61 GKOIVQEILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120  
QY 121 QAIMDKNIIKANFSVIFERLETLILLRAFTTEGAIVGEISPLSPGHTNEDVKNAIGV 180  
DB 121 QAIMDKNIIKANFSVIFERLETLILLRAFTTEGAIVGEISPLSPGHTNEDVKNAIGV 180  
QY 181 LGGLKNDNTVRISSETLQRFAMRSSHENGSRPFPKQKRMERTIEPEV 230  
DB 181 LGGLKNDNTVRISSETLQRFAMRSSHENGSRPFPKQKRMERTIEPEV 230

RESULT 3  
nonstructural protein NS1 - influenza A virus (strain A/pintail/Alberta/119/79)  
C:Species: influenza A virus  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
C:Accession: G32662  
R:Frederick, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.  
Virology 171, 1-9, 1989  
A:Title: The B allele of the NS gene of avian influenza viruses, but not the A allele,  
A:Reference number: A32662; MUID:89299445; PMID:2525836  
A:Accession: G32662  
A:Molecule type: genomic RNA  
A:Residues: 1-230 <TRE>  
A:Cross-references: UNIPROT:P13140; UNIPARC:UPI0000174ABC  
C:Genetics: NS1  
A:Map position: segment 8  
C:Superfamily: influenza virus nonstructural protein NS1  
C:Keywords: alternative splicing; nonstructural protein

Query Match 92.8%; Score 1093; DB 1; Length 230;  
Best Local Similarity 92.2%; Pred. No. 9e-86; 9; Indels 0; Gaps 0;

QY 1 MDSNTVSSSFQVDCFLWHVRRKRFADQELGDAPFLDLRRDQSLKGRGSLGLDITATRA 60  
DB 1 MDSNTVSSSFQVDCFLWHVRRKRFADQELGDAPFLDLRRDQSLKGRGSLGLDITATRA 60  
QY 61 GKOIVQEILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120  
DB 61 GKOIVQEILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120  
QY 121 QAIMDKNIIKANFSVIFERLETLILLRAFTTEGAIVGEISPLSPGHTNEDVKNAIGV 180  
DB 121 QAIMDKNIIKANFSVIFERLETLILLRAFTTEGAIVGEISPLSPGHTNEDVKNAIGV 180  
QY 181 LGGLKNDNTVRISSETLQRFAMRSSHENGSRPFPKQKRMERTIEPEV 230  
DB 181 LGGLKNDNTVRISSETLQRFAMRSSHENGSRPFPKQKRMERTIEPEV 230

RESULT 4  
nonstructural protein NS1 - influenza A virus (strain A/pintail/Alberta/119/79)  
C:Species: influenza A virus  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
C:Accession: G32662  
R:Frederick, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.  
Virology 171, 1-9, 1989  
A:Title: The B allele of the NS gene of avian influenza viruses, but not the A allele,  
A:Reference number: A32662; MUID:89299445; PMID:2525836  
A:Accession: G32662  
A:Molecule type: genomic RNA  
A:Residues: 1-230 <TRE>  
A:Cross-references: UNIPROT:P13140; UNIPARC:UPI0000174ABC  
C:Genetics: NS1  
A:Map position: segment 8  
C:Superfamily: influenza virus nonstructural protein NS1  
C:Keywords: alternative splicing; nonstructural protein





C;Keywords: alternative splicing; nonstructural protein

Query Match 89.6%; Score 1055; DB 1; Length 237;  
Best Local Similarity 88.3%; Pred. No. 1.6e-82;  
Matches 203; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLMHVVRKFPADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATRA 60  
DB 1 MDNTVSSFOVDCFLMHVVRKQVADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATCV 60  
QY 61 GKQIVQILLESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQVTSGLCIRMD 120  
DB 61 GKQIVVERILKEESDEALKMTIASAPASRYLTDMLTEEMSRDWMFMPKQVAGPLCIRMD 120  
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTGAGVGEISPLSPGHTNEDVKNAIGV 180  
DB 121 QAIMDKNIIILKANFSVIFDRLETLILLRAFTGAGVGEISPLSPGHTNEDVKNAIGV 180  
QY 181 LIGGLKWNNTVRISSETLQRFARSSHENGSRPFPKQKRWERTIEPEV 230  
DB 181 LIGGLEWNTVRVSKTLQRFARSSNENGRPPLTPKQKRWARTIRSEV 230

## RESULT 10

MNIVX7 nonstructural protein NS1 - influenza A virus (strain A/Duck/Ukraine/63 [H3N8]) (fragment

C;Species: influenza A virus  
C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 16-Jul-1999  
C;Accession: G27846  
R;Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.

A;Title: Genetic divergence of the NS genes of avian influenza viruses.  
A;Reference number: A94361; MUID:87236215; PMID:2954302

A;Accession: G27846

A;Molecule type: genomic RNA

A;Residues: 1-227 <NA>

A;Cross-references: UNIPARC:UPI000138A55; GB:M16565; NID:G324789; PIDN:AAA43512.1; PID:

C;Genetics:

A;Gene: NS1

A;Map position: segment 8

A;Superfamily: influenza virus nonstructural protein NS1

C;Keywords: alternative splicing; nonstructural protein

Query Match 89.5%; Score 1054; DB 1; Length 227;  
Best Local Similarity 89.9%; Pred. No. 1.9e-82;  
Matches 204; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 4 NTVSSFOVDCFLMHVVRKFPADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATRAKQ 63  
DB 1 NTVSSFOVDCFLMHVVRKFPADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATRAKQ 60  
QY 64 IVEQILLESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQVTSGLCIRMDQAI 123  
DB 61 TVERILEEFDEVLKMTIASGPASRYLTDMLTEEMSRDWMFMPKQVAGSLCIRMDQAI 120  
QY 124 MDKNIIILKANFSVIFERLETLILLRAFTGAGVGEISPLSPGHTNEDVKNAIGVLIG 183  
DB 121 MDKDIILKANFSVIFNRLETLILLRAFTGAGVGEISPLSPGHTNEDVKNAIGDLIG 180  
QY 184 GLKWNNTVRISSETLQRFARSSHENGSRPFPKQKRWERTIEPEV 230  
DB 181 GLEWNTVRVSETLQRFARSSNEDGRPPLTPKQKRWARTIESEV 227

## RESULT 11

MNIV14

nonstructural protein NS1 - influenza A virus (strain A/FW/1/50 [H1N1])

C;Species: influenza A virus

C;Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 16-Jul-1999

C;Accession: A92991; A04090; B92982

R;Krystal, M.; Buonagurio, D.; Young, J.F.; Palese, P.

J. Virol. 45, 547-554, 1983

A;Title: Sequential mutations in the NS genes of influenza virus field strains.

A;Reference number: A92991; MUID:83164298; PMID:6834468

A;Accession: A92991

A;Molecule type: Genomic RNA

A;Residues: 1-237 <KRY>

A;Cross-references: UNIPARC:UPI0000138A57; GB:K00576; NID:G324813; PIDN:AAA43525.1; PID:

C;Genetics:

A;Map position: segment 8

A;Superfamily: influenza virus nonstructural protein NS1

C;Keywords: alternative splicing

Query Match 89.5%; Score 1054; DB 1; Length 237;  
Best Local Similarity 88.3%; Pred. No. 2e-82;  
Matches 203; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLMHVVRKFPADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATRA 60  
DB 1 MDNTVSSFOVDCFLMHVVRKQVADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATRV 60  
QY 61 GKQIVQILLESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQVTSGLCIRMD 120  
DB 61 GKQIVVERILKEESDEALKMTIASAPASRYLTDMLTEEMSRDWMFMPKQVAGPLCIRMD 120  
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTGAGVGEISPLSPGHTNEDVKNAIGV 180  
DB 121 QAIMDKNIIILKANFSVIFDRLETLILLRAFTGAGVGEISPLSPGHTNEDVKNAIGV 180  
QY 181 LIGGLKWNNTVRISSETLQRFARSSHENGSRPFPKQKRWERTIEPEV 230  
DB 181 LIGGLEWNTVRVSKTLQRFARSSNENGRPPLTPKQKRWARTIRSEV 230

## RESULT 12

MNIV77

nonstructural protein NS1 - influenza A virus (strain A/USSR/90/77 [H1N1])

C;Species: influenza A virus

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 16-Jul-1999

C;Accession: E92991; A04090

J;Krystal, M.; Buonagurio, D.; Young, J.F.; Palese, P.

R. Virol. 45, 547-554, 1983

A;Title: Sequential mutations in the NS genes of influenza virus field strains.

A;Reference number: A92991; MUID:83164298; PMID:6834468

A;Accession: E92991

A;Molecule type: genomic RNA

A;Residues: 1-237 <KRY>

A;Cross-references: UNIPARC:UPI0000138A66; GB:K00578; NID:G324839; PIDN:AAA43540.1; PID:

C;Genetics:

A;Map position: segment 8

A;Superfamily: influenza virus nonstructural protein NS1

C;Keywords: alternative splicing

Query Match 89.4%; Score 1053; DB 1; Length 237;  
Best Local Similarity 88.3%; Pred. No. 2.4e-82;  
Matches 203; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLMHVVRKFPADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATRA 60  
DB 1 MDNTVSSFOVDCFLMHVVRKQVADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATCV 60  
QY 61 GKQIVQILLESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQVTSGLCIRMD 120  
DB 61 GKQIVVERILKEESDEALKMTIASAPASRYLTDMLTEEMSRDWMFMPKQVAGPLCIRMD 120  
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTGAGVGEISPLSPGHTNEDVKNAIGV 180  
DB 121 QAIMDKNIIILKANFSVIFDRLETLILLRAFTGAGVGEISPLSPGHTNEDVKNAIGV 180  
QY 181 LIGGLKWNNTVRISSETLQRFARSSHENGSRPFPKQKRWERTIEPEV 230  
DB 181 LIGGLEWNTVRVSKTLQRFARSSNENGRPPLTPKQKRWARTIRSEV 230

## RESULT 13

MNIV1

nonstructural protein NS1 - influenza A virus (strain A/PR/8/34)

C:Species: influenza A virus  
C:Date: 30-Apr-1981 #sequence\_revision 30-Apr-1981 #text\_change 30-Sep-1993  
C:Accession: A04089  
R:Baer, M.; Taussig, R.; Zazza, J.J.; Young, J.F.; Palese, P.; Reisfeld, A.; Skalka, A.M.  
Nucleic Acids Res. 8, 5845-5858, 1980  
A:Title: Complete nucleotide sequence of the influenza A/PR/8/34 virus NS gene and complete coding region  
A:Reference number: A93714; MUID:81124304; PMID:7465426  
A:Accession: A04089  
A:Molecule type: genomic RNA  
A:Residues: 1-230 <BAE>  
A:Cross-references: UNIPARC:UPI00000016F6  
C:Genetics:  
A:Map position: segment 8  
C:Superfamily: influenza virus nonstructural protein NS1  
C:Keywords: alternative splicing

Query Match 89.3%; Score 1052; DB 1; Length 230;  
Best Local Similarity 88.7%; Pred. No. 2.8e-82;  
Matches 204; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLMHWKRFADQELGDAPFLDRLRRDQSLKGRGSTLGLDIETATRA 60  
DB 1 MDPNTVSSFOVDCFLMHWKRFADQELGDAPFLDRLRRDQSLKGRGSTLGLDIETATRA 60  
QY 61 GKQIVQEILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120  
DB 61 GKQIVQEILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120  
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAGV 180  
DB 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAGV 180  
QY 181 LIGGLEWNTVRSVETLQRFARSSSHENGSRPFPKQKRMERTIEPEV 230  
DB 181 LIGGLEWNTVRSVETLQRFARSSSHENGSRPFPKQKRMERTIEPEV 230

## RESULT 14

## MNIVX1

nonstructural protein NS1 - influenza A virus (strain A/Chicken/Japan/24 [H7N7]) (fragment)  
C:Species: influenza A virus  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 16-Jul-1999  
C:Accession: A27846  
R:Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.  
Virology 158, 465-468, 1987  
A:Title: Genetic divergence of the NS genes of avian influenza viruses.  
A:Reference number: A94361; MUID:87236215; PMID:2954302  
A:Accession: A27846  
A:Molecule type: genomic RNA  
A:Residues: 1-227 <NAK>  
A:Cross-references: UNIPARC:UPI0000138A52; GB:M16561; NID:g324777; PID:AAA43504.1; PID:  
C:Genetics:  
A:Gene: NS1  
A:Map position: segment 8  
C:Superfamily: influenza virus nonstructural protein NS1  
C:Keywords: alternative splicing; nonstructural protein

Query Match 89.2%; Score 1051; DB 1; Length 227;

Best Local Similarity 90.3%; Pred. No. 3.4e-82;  
Matches 205; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 4 NTSSSFQVDCFLMHWKRFADQELGDAPFLDRLRRDQSLKGRGSTLGLDIETATRA 63  
DB 1 NTSSSFQVDCFLMHWKRFADQELGDAPFLDRLRRDQSLKGRGSTLGLDIETATRA 60  
QY 64 IVEQILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMDQAI 123  
DB 61 IVEQILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMDQAI 120  
QY 124 MDKNIIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAGV 183  
DB 121 MDKNIIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAGV 180

QY 184 GLKWNNTVRSVETLQRFARSSSHENGSRPFPKQKRMERTIEPEV 230  
DB 181 GLEWNTVRSVETLQRFARSSSHENGSRPFPKQKRMERTIESEV 227

## RESULT 15

## S09648

nonstructural protein NS1 - influenza A virus (strain A/Leningrad/1/54)  
C:Species: influenza A virus  
C:Date: 21-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 19-May-2000  
C:Accession: S09648  
R:Beklemishev, A.B.; Blinov, V.M.; Vassilenko, S.K.; Golovin, S.Y.; Karginov, V.A.; Mama  
Bioorg. Khim. 11, 641-645, 1985  
A:Title: Synthesis, cloning and sequencing of a full-length DNA copy of the fragment 8 c  
A:Reference number: S09648; MUID:85307107; PMID:4038350  
A:Accession: S09648  
A:Status: preliminary; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-230 <BEK>  
A:Cross-references: UNIPARC:UPI0000000533; EMBL:X52146; NID:g60716; PIDN:CAA36392.1; PID:  
C:Superfamily: influenza virus nonstructural protein NS1

Query Match 89.0%; Score 1048; DB 2; Length 230;

Best Local Similarity 88.3%; Pred. No. 6.2e-82;  
Matches 203; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLMHWKRFADQELGDAPFLDRLRRDQSLKGRGSTLGLDIETATRA 60  
DB 1 MDPNTVSSFOVDCFLMHWKRFADQELGDAPFLDRLRRDQSLKGRGSTLGLDIETATRA 60  
QY 61 GKQIVQEILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120  
DB 61 GKQIVQEILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120  
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAGV 180  
DB 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAGV 180

QY 181 LIGGLEWNTVRSVETLQRFARSSSHENGSRPFPKQKRMERTIEPEV 230

DB 181 LIGGLEWNTVRSVETLQRFARSSSHENGSRPFPKQKRMERTIESEV 230

Search completed: March 7, 2006, 19:21:49

Job time : 41 secs

**This Page Blank (uspto)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2006, 19:13:44 ; Search time 186 Seconds  
(without alignments)  
543.318 Million cell updates/sec

Title: US-10-734-373-58  
Perfect score: 1178  
Sequence: 1 MDSNTVSSQVDCFLWVRK.....RPSFPPKOKRMERTIEREV 230

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

A\_Geneseq\_21.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*
- 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1178	100.0	230	4	Aae09027 Equine in
2	1178	100.0	230	4	Aae09029 Equine in
3	1165	98.9	230	2	Aaw03522 Non-struct
4	1099	93.3	230	8	Ado14175 Influenza
5	1083	91.9	227	8	Ado14179 Influenza
6	1066	90.5	227	8	Ado14177 Influenza
7	1066	90.5	230	8	Ado14174 Influenza
8	1061	90.1	238	9	Ady62119 Influenza
9	1059	89.9	230	8	Ado14183 Influenza
10	1055	89.6	237	5	Aae23116 Influenza
11	1052	89.3	230	9	Ady62121 Mutant In
12	1051	89.2	227	8	Ado14180 Influenza
13	1048	89.0	230	8	Ado14171 Influenza
14	1042	88.5	230	8	Ado14176 Influenza
15	1017	85.7	237	5	Abb05772 Influenza
16	1007	85.5	217	8	Ado14178 Influenza
17	953	80.9	202	8	Ado14184 Influenza
18	856	72.7	230	8	Ado14172 Influenza
19	852	72.3	230	8	Ado14181 Influenza
20	789	67.0	173	8	Ado14173 Influenza
21	586	49.7	193	9	Adv90024 Caspase c
22	488	41.4	97	4	Aae09028 Equine in
23	429	36.4	124	8	Ado14182 Influenza
24	400.5	34.0	246	2	Aaw12714 Flu NS1-H

25	400	34.0	344	4	ABU71886
26	395	33.5	231	2	AAR20301
27	392.5	33.3	306	2	AAR38867
28	392.5	33.3	306	2	AAR38867
29	390.5	33.1	337	2	AAR33448
30	389.5	33.1	230	2	AAR38868
31	389.5	33.1	230	2	AAR38868
32	389.5	33.1	230	2	AAR60195
33	389.5	33.1	230	2	AAR60226
34	389.5	33.1	304	2	AAR60197
35	388	32.9	309	2	AAR60207
36	388	32.9	319	2	AAR13175
37	388	32.9	319	2	AAR13176
38	388	32.9	327	2	AAR13177
39	387.5	32.9	225	2	AAR38879
40	387.5	32.9	225	2	AAR60217
41	387.5	32.9	231	2	AAR38878
42	387.5	32.9	231	2	AAR60216
43	387.5	32.9	242	2	AAR04208
44	387.5	32.9	242	2	AAR60209
45	387	32.9	312	4	AAY72521

## ALIGNMENTS

## RESULT 1

Aae09027

ID AAE09027 standard; protein; 230 AA.

XX AAE09027;

XX AC

XX AAE09027;

XX 15-NOV-2001 (first entry)

XX Equine influenza virus H3N8 PeiwtlNS230 protein.

XX Equine influenza virus; ei; cold adaptation; temperature sensitivity;

XX KW vaccine; neiwtlNS891 DNA; PeiwtlNS230 protein.

XX OS Equine influenza virus H3N8.

XX WO200160849-A2.

XX PD 23-AUG-2001.

XX PF 16-FEB-2001; 2001WO-US005048.

XX PR 16-FEB-2000; 2000US-00506286.

XX (UYPI-) UNIV PITTSBURGH.

XX PA Dowling PW, Youngner JS;

XX WPI; 2001-522584/57.

XX DR N-PSDB; AADI5678.

XX Novel isolated equine influenza virus (wild-type and cold-adapted) proteins and viruses containing nucleic acid molecules encoding the proteins, which are useful for protecting animals from influenza virus infections.

XX Claim 5; Page 72-73; 172pp; English.

XX The patent discloses cold-adapted equine influenza viruses and reassortant influenza A viruses comprising atleast one genome segment of such an equine influenza virus, wherein the equine influenza virus genome segment confers atleast one identifying phenotype of the cold-adapted equine influenza virus, such as cold adaptation, temperature sensitivity, dominant interference or attenuation. The viruses are useful for protecting animals from diseases caused by influenza viruses. They are also used as vaccines. The present sequence is an equine influenza (ei) virus H3N8 Peiwtl (wild type) NS230 protein which is encoded by neiwtlNS891 DNA

```

XX Sequence 230 AA;
Query Match 100.0%; Score 1178; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 9.3e-118;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSNTVSSFOVDCFLWHVVRKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDLETATRA 60
DB 1 MDSNTVSSFOVDCFLWHVVRKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDLETATRA 60
QY 61 GKQIVQIILEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVQIILEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILRAFTTEGAVGVEISPLPSLPGHTNEDVKNAIGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILRAFTTEGAVGVEISPLPSLPGHTNEDVKNAIGV 180
QY 181 LIGLKWNDNTVRISETLQRFARSSHENGSRPSPPKQKRMERTIEPEV 230
DB 181 LIGLKWNDNTVRISETLQRFARSSHENGSRPSPPKQKRMERTIEPEV 230

RESULT 2
AAE09029
ID AAE09029 standard; protein; 230 AA.
AC AAE09029;
XX
XX
XX 15-NOV-2001 (first entry)
XX
XX Equine influenza virus H3N8 PeicalNS230 protein.
XX
XX Equine influenza virus; ei; cold adaptation; temperature sensitivity;
XX vaccine; neicalNS888 DNA; PeicalNS230 protein.
XX
XX Equine influenza virus H3N8.
XX
XX WO200160849-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005048.
XX
XX 16-FEB-2000; 2000US-00506286.
XX
XX (UYP1-) UNIV PITTSBURGH.
XX
XX Dowling PW, Youngner JS;
XX
XX WPI: 2001-522584/57.
XX
XX N-PSDB; AAD15681.
XX
XX Novel isolated equine influenza virus (wild-type and cold-adapted)
XX proteins and viruses containing nucleic acid molecules encoding the
XX proteins, which are useful for protecting animals from influenza virus
XX infections.
XX
XX Claim 5; Page 77; 172pp; English.
XX
XX The patent discloses cold-adapted equine influenza viruses and
XX reassortant influenza A viruses comprising atleast one genome segment of
XX such an equine influenza virus, wherein the equine influenza virus genome
XX segment confers atleast one identifying phenotype of the cold-adapted
XX equine influenza virus, such as cold adaptation, temperature sensitivity,
XX dominant interference or attenuation. The viruses are useful for
XX protecting animals from diseases caused by influenza viruses. They are
XX also used as vaccines. The present sequence is equine influenza (ei)
XX virus H3N8 Peical (cold adapted) NS230 protein which is encoded by
XX neicalNS888 DNA
XX
XX Sequence 230 AA;

```

```

Query Match 100.0%; Score 1178; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 9.3e-118;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSNTVSSFOVDCFLWHVVRKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDLETATRA 60
DB 1 MDSNTVSSFOVDCFLWHVVRKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDLETATRA 60
QY 61 GKQIVQIILEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVQIILEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILRAFTTEGAVGVEISPLPSLPGHTNEDVKNAIGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILRAFTTEGAVGVEISPLPSLPGHTNEDVKNAIGV 180
QY 181 LIGLKWNDNTVRISETLQRFARSSHENGSRPSPPKQKRMERTIEPEV 230
DB 181 LIGLKWNDNTVRISETLQRFARSSHENGSRPSPPKQKRMERTIEPEV 230

RESULT 3
AAW03522
ID AAW03522 standard; protein; 230 AA.
XX
XX
XX AAW03522;
XX
XX 16-OCT-2003 (revised)
XX
XX 09-APR-1997 (first entry)
XX
XX Non-structural protein NS1 of influenza A virus.
XX
XX Non-structural protein; NS1; influenza virus; respiratory tract;
XX diagnosis; anti-NS1 antibody; primer; PCR; detection; amplify.
XX
XX Influenza virus; A/equine 1/Suffolk 89.
XX
XX EP726316-A2.
XX
XX 14-AUG-1996.
XX
XX 31-JAN-1996; 96EP-00300681.
XX
XX 09-FEB-1995; 95GB-00002489.
XX
XX (ANIM-) ANIMAL HEALTH TRUST.
XX
XX Binns M, Birch-Machin I;
XX
XX WPI: 1996-364394/37.
XX
XX N-PSDB; AAT37435.
XX
XX Recombinant equine influenza virus NS1 protein - useful for diagnosis of
XX equine influenza A.
XX
XX Example; Fig 1A; 20pp; English.
XX
XX This sequence represents non-structural protein NS1 of influenza virus
XX A/equine 2/Suffolk 89. The NS1 protein is useful for diagnosis of equine
XX influenza A infections by detection of anti-NS1 antibodies. The NS1
XX coding sequence was isolated using the primer sequences given in AAT37436
XX -40. (Updated on 16-OCT-2003 to standardise OS field)
XX
XX Sequence 230 AA;
Query Match 98.9%; Score 1165; DB 2; Length 230;
Best Local Similarity 98.7%; Pred. No. 2.3e-116;
Matches 227; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDSNTVSSFOVDCFLWHVVRKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDLETATRA 60
DB 1 MDSNTVSSFOVDCFLWHVVRKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDLETATRA 60

```

QY 61 GKQIVQIIEEESDEALKMTIASVPASRYLDTMTLDEMSTRDWFMLMPKQKVTGSLCIRMD 120  
DB 61 GKQIVQIIEEESDEAFKMTIASVPASRYLDTMTLDEMSTRDWFMLMPKQKVTGSLCIRMD 120  
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTEGAVVGEISPLSPGHTNEDVKNAIGV 180  
DB 121 QAIMDKNIILKANFSVIFERLETLILLRAFTEGAVVGEISPLSPGHTNEDVKNAIGV 180  
QY 181 LIGGLKWNNDTVRISETLQRFWRSHENGSRPFPKQKQMERTIEPEV 230  
DB 181 LIGGLKWNNDTVRVSETLQRFWRSHENGSRPFPKQKQMERTIESEV 230

RESULT 4  
ADO14175  
ID ADO14175 standard; protein; 230 AA.  
XX  
AC ADO14175;  
DT 12-AUG-2004 (first entry)  
XX  
DE Influenza A virus non-structural protein (NS)-1 #5.  
XX  
KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;  
KW double-stranded RNA; dsRNA; binding domain; virucide;  
KW double-stranded-RNA-activated protein kinase; phosphorylation;  
KW translation inhibition factor; eIF2alpha; viral protein synthesis;  
KW viral protein replication; screening method; infection.  
XX  
OS Influenza A virus.  
XX  
PN WO2004043404-A2.  
XX  
PD 27-MAY-2004.  
XX  
PF 13-NOV-2003; 2003WO-US036292.  
XX  
PR 13-NOV-2002; 2002US-0425661P.  
PR 10-JUN-2003; 2003US-0477453P.  
XX  
PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
XX  
PI Montelione GT, Krug RM;  
XX  
PI WPI; 2004-420083/39.  
XX

This invention relates to a novel method of identifying an inhibitor of influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus non-structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding domain and a dsRNA that binds the protein. The invention may be useful for the production of compounds with a virucide activity acting as inhibitors of binding between influenza virus non-structural protein-1 (NS1) and double-stranded RNA. It is possible that binding of double-stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA-activated protein kinase to remain in an inactive state so that it does not catalyze the phosphorylation of translation inhibition factor eIF2alpha, which would otherwise inhibit viral protein synthesis and replication. The invention is useful as a (high throughput) screening method for identifying compounds having inhibitory activity against influenza virus. Compounds identified are useful in treating animals, including human infected with influenza virus. The present sequence is that of an influenza virus non-structural (NS)-1 protein which is related to the method of the invention.

This invention relates to a novel method of identifying an inhibitor of influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus non-structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding domain and a dsRNA that binds the protein. The invention may be useful for the production of compounds with a virucide activity acting as inhibitors of binding between influenza virus non-structural protein-1 (NS1) and double-stranded RNA. It is possible that binding of double-stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA-activated protein kinase to remain in an inactive state so that it does not catalyze the phosphorylation of translation inhibition factor eIF2alpha, which would otherwise inhibit viral protein synthesis and replication. The invention is useful as a (high throughput) screening method for identifying compounds having inhibitory activity against influenza virus. Compounds identified are useful in treating animals, including human infected with influenza virus. The present sequence is that of an influenza virus non-structural (NS)-1 protein which is related to the method of the invention.

SQ Sequence 230 AA;  
Query Match 93.3%; Score 1099; DB: 8; Length 230;  
Best Local Similarity 92.6%; Pred. No. 2.9e-109;  
Matches 213; Conservative 11; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MDSNTVSSQVDCFLWVHRKFAADQELGDAPFLDLRLRDQKSLKGRSGTGLDIEATRA 60  
DB 1 MDSNTVSSQVDCFLWVHRKFAADQELGDAPFLDLRLRDQKSLKGRSGTGLDIEATCA 60  
QY 61 GKQIVQIIEEESDEALKMTIASVPASRYLDTMTLDEMSTRDWFMLMPKQKVTGSLCIRMD 120  
DB 61 GKQIVQIIEEESDEALKMTIASVPASRYLDTMTLDEMSTRDWFMLMPKQKVTGSLCIRMD 120  
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTEGAVVGEISPLSPGHTNEDVKNAIGV 180  
DB 121 QAIMDKNIILKANFSVIFERLETLILLRAFTEGAVVGEISPLSPGHTNEDVKNAIGV 180  
QY 181 LIGGLKWNNDTVRISETLQRFWRSHENGSRPFPKQKQMERTIEPEV 230  
DB 181 LIGGLKWNNDTVRVSETLQRFWRSHENGSRPFPKQKQMERTIESEV 230

RESULT 5  
ADO14175  
ID ADO14175 standard; protein; 227 AA.  
XX  
AC ADO14175;  
DT 12-AUG-2004 (first entry)  
XX  
DE Influenza A virus non-structural protein (NS)-1 #9.  
XX  
KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;  
KW double-stranded RNA; dsRNA; binding domain; virucide;  
KW double-stranded-RNA-activated protein kinase; phosphorylation;  
KW translation inhibition factor; eIF2alpha; viral protein synthesis;  
KW viral protein replication; screening method; infection.  
XX  
OS Influenza A virus.  
XX  
PN WO2004043404-A2.  
XX  
PD 27-MAY-2004.  
XX  
PF 13-NOV-2003; 2003WO-US036292.  
XX  
PR 13-NOV-2002; 2002US-0425661P.  
PR 10-JUN-2003; 2003US-0477453P.  
XX  
PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
XX  
PI Montelione GT, Krug RM;  
XX  
PI WPI; 2004-420083/39.  
XX

Identifying agents useful for treating influenza virus infection comprises identifying compounds that inhibit binding between influenza virus non-structural protein-1 (NS1) and a double-stranded RNA that binds the protein.  
Disclosure; Page 13; 92pp; English.  
This invention relates to a novel method of identifying an inhibitor of influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus non-structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding domain and a dsRNA that binds the protein. The invention may be useful for the production of compounds with a virucide activity acting as inhibitors of binding between influenza virus non-structural protein-1 (NS1) and double-stranded RNA. It is possible that binding of double-stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA-activated protein kinase to remain in an inactive state so that it does

CC not catalyse the phosphorylation of translation inhibition factor  
 CC eIF2alpha, which would otherwise inhibit viral protein synthesis and  
 CC replication. The invention is useful as a (high throughput) screening  
 CC method for identifying compounds having inhibitory activity against  
 CC influenza virus. Compounds identified are useful in treating animals,  
 CC including human infected with influenza virus. The present sequence is  
 CC that of an influenza virus non-structural (NS)-1 protein which is related  
 CC to the method of the invention.

SQ Sequence 227 AA;

Query Match 91.9%; Score 1083; DB 8; Length 227;

Best Local Similarity 92.1%; Pred. No. 1,5e-107; Indels 0; Gaps 0;

Matches 209; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

OY 4 NTVSSFOVDFLWVVKRFADQELGDAPFLDRDQSLKGRGSLGLDLETATRAKQ 63

DB 1 NTVSSFOVDFLWVVKRFADQELGDAPFLDRDQSLKGRGSLGLDLETATRAKQ 60

OY 64 IVFOILEESDEALQMTIASVPASRYLTMTLDESRDWFMLPKQKVTGSLCIRMDQAI 123

DB 61 IVERILVEESDEALQMTIASVPASRYLTMTLDESRDWFMLPKQKVTGSLCIRMDQAI 120

OY 124 MDKNIILKANFSVIFERLETLILIRAFTEGAVGEISPLSPFGHTNEDVKNAIGVLIG 183

DB 121 MDKNIILKANFSVIFERLETLILIRAFTEGAVGEISPLSPFGHTNEDVKNAIGVLIG 180

OY 184 GLKWNNTVRISETLQRPAMRSSHENGSRPFPKQKQKERTIEPEV 230

DB 181 GLEWNDNTVRVSETLQRPAMRSSHENGSRPFPKQKQKERTIEPEV 227

RESULT 6

ADOI4177

ID ADO14177 standard; protein; 227 AA.

AC ADO14177;

XX 12-AUG-2004 (first entry)

DE Influenza A virus non-structural protein (NS)-1 #7.

XX influenza inhibitor; influenza virus; non-structural protein-1; NS1;

KW double-stranded RNA; dsRNA; binding domain; virucide;

KW double-stranded-RNA-activated protein kinase; phosphorylation;

KW translation inhibition factor; eIF2alpha; viral protein synthesis;

XX viral protein replication; screening method; infection.

OS Influenza A virus.

XX WO2004043404-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036292.

XX 13-NOV-2002; 2002US-0425661P.

XX 10-JUN-2003; 2003US-0477453P.

XX (RUTP ) UNIV RUTGERS STATE NEW JERSEY.

XX Montellione GT, Krug RM;

XX WPI; 2004-420083/39.

XX Identifying agents useful for treating influenza virus infection

XX comprises identifying compounds that inhibit binding between influenza

XX virus non-structural protein-1 (NS1) and a double-stranded RNA that binds

XX the protein.

XX Disclosure; Page 13; 92pp; English.

XX This invention relates to a novel method of identifying an inhibitor of

XX

CC

CC influenza virus which comprises testing candidate compounds for their  
 CC ability to reduce the extent of binding between influenza virus non-  
 CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding  
 CC domain and a dsRNA that binds the protein. The invention may be useful  
 CC for the production of compounds with a virucide activity acting as  
 CC inhibitors of binding between influenza virus non-structural protein-1  
 CC (NS1) and double-stranded RNA. It is possible that binding of double-  
 CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA  
 CC -activated protein kinase to remain in an inactive state so that it does  
 CC not catalyse the phosphorylation of translation inhibition factor  
 CC eIF2alpha, which would otherwise inhibit viral protein synthesis and  
 CC replication. The invention is useful as a (high throughput) screening  
 CC method for identifying compounds having inhibitory activity against  
 CC influenza virus. Compounds identified are useful in treating animals,  
 CC including human infected with influenza virus. The present sequence is  
 CC that of an influenza virus non-structural (NS)-1 protein which is related  
 CC to the method of the invention.

SQ Sequence 227 AA;

Query Match 90.5%; Score 1066; DB 8; Length 227;

Best Local Similarity 91.2%; Pred. No. 1e-105;

Matches 207; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

OY 4 NTVSSFOVDFLWVVKRFADQELGDAPFLDRDQSLKGRGSLGLDLETATRAKQ 63

DB 1 NTVSSFOVDFLWVVKRFADQELGDAPFLDRDQSLKGRGSLGLDLETATRAKQ 60

OY 64 IVEOILEESDEALQMTIASVPASRYLTMTLDESRDWFMLPKQKVTGSLCIRMDQAI 123

DB 61 IVERILVEESDEALQMTIASVPASRYLTMTLDESRDWFMLPKQKVTGSLCIRMDQAI 120

OY 124 MDKNIILKANFSVIFERLETLILIRAFTEGAVGEISPLSPFGHTNEDVKNAIGVLIG 183

DB 121 MDKNIILKANFSVIFERLETLILIRAFTEGAVGEISPLSPFGHTNEDVKNAIGVLIG 180

OY 184 GLKWNNTVRISETLQRPAMRSSHENGSRPFPKQKQKERTIEPEV 230

DB 181 GLEWNDNTVRVSETLQRPAMRSSHENGSRPFPKQKQKERTIEPEV 227

RESULT 7

ADOI4174

ID ADO14174 standard; protein; 230 AA.

AC ADO14174;

XX 12-AUG-2004 (first entry)

DE Influenza A virus non-structural protein (NS)-1 #4.

XX influenza inhibitor; influenza virus; non-structural protein-1; NS1;

KW double-stranded RNA; dsRNA; binding domain; virucide;

KW double-stranded-RNA-activated protein kinase; phosphorylation;

KW translation inhibition factor; eIF2alpha; viral protein synthesis;

XX viral protein replication; screening method; infection.

OS Influenza A virus.

XX WO2004043404-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036292.

XX 13-NOV-2002; 2002US-0425661P.

XX 10-JUN-2003; 2003US-0477453P.

XX (RUTP ) UNIV RUTGERS STATE NEW JERSEY.

XX Montellione GT, Krug RM;

XX WPI; 2004-420083/39.

XX

CC





KW translation inhibition factor; eIF2alpha; viral protein synthesis;  
KW viral protein replication; screening method; infection.  
OS Influenza A virus; A/Turkey/Oregon/71 (H7).  
XX WO2004043404-A2.  
XX 27-MAY-2004.  
XX 13-NOV-2003; 2003WO-US036292.  
XX 13-NOV-2002; 2002US-0425661P.  
XX 10-JUN-2003; 2003US-0477453P.  
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
XX Montelione GT, Krug RM;  
XX WPI; 2004-420083/39.  
XX Identifying agents useful for treating influenza virus infection  
PT comprises identifying compounds that inhibit binding between influenza  
PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds  
PT the protein.  
XX Disclosure; Page 14; 92pp; English.  
XX This invention relates to a novel method of identifying an inhibitor of  
CC influenza virus which comprises testing candidate compounds for their  
CC ability to reduce the extent of binding between influenza virus non-  
CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding  
CC domain and a dsRNA that binds the protein. The invention may be useful  
CC for the production of compounds with a virucide activity acting as  
CC inhibitors of binding between influenza virus non-structural protein-1  
CC (NS1) and double-stranded RNA. It is possible that binding of double-  
CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA  
CC -activated protein kinase to remain in an inactive state so that it does  
CC not catalyse the phosphorylation of translation inhibition factor  
CC eIF2alpha, which would otherwise inhibit viral protein synthesis and  
CC replication. The invention is useful as a (high throughput) screening  
CC method for identifying compounds having inhibitory activity against  
CC influenza virus. Compounds identified are useful in treating animals,  
CC including human infected with influenza virus. The present sequence is  
CC that of an influenza virus non-structural (NS)-1 protein which is related  
CC to the method of the invention.  
XX Sequence 230 AA;

Query Match 89.9%; Score 1059; DB 8; Length 230;  
Best Local Similarity 88.7%; Pred. No. 5.8e-105;  
Matches 204; Conservative 12; Mismatches 14; Indels 0; Gaps 0;  
QY 1 MDSNTVSSFOVDCFLWHVRRKRFADQELGDAPFLDRLRRDQKSLKGRGSLGLDITATRA 60  
DB 1 MDSNTVSSFOVDCFLWHVRRKRFADQELGDAPFLDRLRRDQKSLKGRGSLGLDITATRE 60  
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDEMRSDFWMLMPKQKVTGSLCIRMD 120  
DB 61 GKQIVERILEESDEALKMTIASVPASRYLTDMTLEMSRDLMLIPKQKVTGSLCIRMD 120  
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTEGAVGVEISPLPSLPCHTNEDEVKNAIGV 180  
DB 121 QAVMGKTIILKANFSVIFNRLEALILLRAFTDEGALVGEISPLPSLPCHTNEDEVKNAIGV 180  
QY 181 LIGGLKWNNDTVRISETLQRFWRSSHENGSPFPKQKRMERTIEPEV 230  
DB 181 LIGGLEWNDTVRVSETLQRTWRSSENGRSPFPKQKRVETIEPEV 230

RESULT 10  
AAE23116  
ID AAE23116 standard; protein; 237 AA.  
XX

AC AAE23116;  
XX 21-AUG-2002 (first entry)  
XX Influenza A virus/singapore/1/57/ca NS1 mutant protein.  
XX Attenuated influenza vaccine; prophylactic; therapeutic; infection;  
XX virucide; mutant; mutein; NS1 protein.  
XX Influenza A virus.  
XX Synthetic.  
XX WO200224876-A2.  
XX 28-MAR-2002.  
XX 25-SEP-2001; 2001WO-EP011087.  
XX 25-SEP-2000; 2000EP-00120896.  
XX (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.  
XX Katinger H, Egorov A, Ferkov B, Romanova J, Katinger D;  
XX WPI; 2002-416282/44.  
XX N-PSDB; AAD37061.  
XX Manufacturing live vaccine, by infecting Vero cells with virus, combining  
PT cells with serum-free cell culture medium, incubating cells in presence  
PT of protease and nuclease, harvesting virus and preparing vaccine.  
XX Example 4; Page 62-63; 90pp; English.  
XX The present invention relates to a method for isolating viruses from  
CC various sources and for producing live attenuated influenza vaccines in a  
CC serum-free African Green monkey kidney (Vero) cell culture under  
CC conditions where alterations in the surface antigens of the virus due to  
CC adaptive selection are minimised or prevented. The method is useful for  
CC the manufacture of whole-virus vaccine, preferably attenuated live  
CC vaccine. It is useful for prophylactic or therapeutic administration  
CC against viral infection, preferably influenza virus infections. The  
CC present sequence is Influenza A virus/singapore/1/57/ca (cold adapted)  
CC NS1 mutant protein. This sequence is used in the exemplification of the  
CC invention  
XX Sequence 237 AA;

Query Match 89.6%; Score 1055; DB 5; Length 237;  
Best Local Similarity 87.8%; Pred. No. 1.6e-104;  
Matches 202; Conservative 17; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MDSNTVSSFOVDCFLWHVRRKRFADQELGDAPFLDRLRRDQKSLKGRGSLGLDITATRA 60  
DB 1 MDPNTVSSFOVDCFLWHVRRKQVADQELGDAPFLDRLRRDQKSLRGRGSLGLNIETATRV 60  
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDEMRSDFWMLMPKQKVTGSLCIRMD 120  
DB 61 GKQIVERILEESDEALKMTIASVPASRYLTDMTLEMSRDLMLIPKQKVTGSLCIRMD 120  
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTEGAVGVEISPLPSLPCHTNEDEVKNAIGV 180  
DB 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTEGAVGVEISPLPSLPCHTNEDEVKNAIGV 180  
QY 181 LIGGLKWNNDTVRISETLQRFWRSSHENGSPFPKQKRMERTIEPEV 230  
DB 181 LIGGLEWNDTVRVSETLQRFWRSSHENGSPFPKQKRVETIEPEV 230

RESULT 11  
ADY62121  
ID ADY62121 standard; protein; 230 AA.  
XX  
AC ADY62121;

XX DT 19-MAY-2005 (first entry)

XX DE Mutant Influenza A virus strain A/England/1/53v-a NS1 protein.

XX KW protein engineering; immune stimulation; immunostimulant; vaccine;

XX KW Influenza virus infection; mutin.

XX OS Influenza A virus; strain A/England/1/53v-a.

XX FH Key Location/Qualifiers

XX FT Misc-difference 21

XX FT FT /note= "replaces Gln in wild type protein"

XX FT FT Misc-difference 58

XX FT FT /note= "replaces Thr in wild type protein"

XX FT FT Misc-difference 60

XX FT FT /note= "replaces Val in wild type protein"

XX FT FT Misc-difference 127

XX FT FT /note= "replaces Asn in wild type protein"

XX FT FT Misc-difference 174

XX FT FT /note= "replaces Val in wild type protein"

XX FT FT Misc-difference 189

XX FT FT /note= "replaces Asp in wild type protein"

XX PN US2005054846-A1.

XX PD 10-MAR-2005.

XX PF 04-SEP-2003; 2003US-00654737.

XX PR 04-SEP-2003; 2003US-00654737.

XX PA (WEBSTER) WEBSTER R G.

XX PA (WEBB) WEBB R J.

XX PA (OZAKI) OZAKI H.

XX PI Webster RG, Webby RJ, Ozaki H;

XX PN WPI: 2005-213104/22.

XX DR N-PSDB; ADY62118.

XX XX

XX PT Producing a reassortant influenza virus that gives a high titer in Vero cells (certified for use in vaccine-production), comprises replacing the NS gene of the A/PuertoRico/3/24 master strain with the NS gene of the A/England/1/53 strain.

XX PS Claim 6; SEQ ID NO 5; 16pp; English.

XX CC The invention relates to a method of producing a high titer reassortant influenza virus by transfecting host cells with expression plasmids containing the PB2, PB1, PA, NP, and M genes from the A/PuertoRico/9/34 influenza strain, the NS gene from the A/England/1/53 influenza strain, and the HA and NA genes from an influenza virus of interest other than A/England/1/53, to obtain a high titer reassortant influenza virus. The method is useful for producing a high titer reassortant influenza virus. The high titer reassortant influenza viruses are useful for producing vaccine compositions. The vaccines are useful for treating or preventing influenza viral infections. Genetic engineering techniques allow the rapid production of custom made attenuated virus vaccines, but vaccine use is limited by the need to use vaccine approved cell lines. The master strain A/PuertoRico/8/34 which is the most widely used in producing recombinant viruses for vaccine use produces a high titer in MDCK cells, which are not certified for use in production of human vaccines, but not in Vero cells, which are certified for this use. The applicants have discovered that replacing the NS gene of the A/PuertoRico/3/24 master strain with the NS gene of the A/England/1/53 strain gives reassortant virus that produces a high titer in Vero cells. This sequence corresponds to the mutated NS1 protein from the A/England/1/53v-a influenza strain.

XX CC Sequence 230 AA;

Query Match 89.3%; Score 1052; DB 9; Length 230;

Best Local Similarity 87.8%; Fred. No. 3.3e-104;

Matches 202; Conservative 16; Mismatches 12; Indels 0; Gaps 0;

QY 1 MDSNTVSPQVDFLWVRKRFADQELGADPDLRLRRDOKSLKGRGSLGLDIAETATRA 60

DB 1 MDPNTVSPQVDFLWVRKRVADQELGADPDLRLRRDOKSLKGRGSLGLNIAETARA 60

QY 61 GKQIVBOILREESDEALKMTIASVPASRYLTDMTLDEMSEDFWMLPKOKVTSGLCIKMD 120

DB 61 GKQIVBOILREESDEALKMTIASVPASRYLTDMTLDEMSEDFWMLPKOKVTSGLCIKMD 120

QY 121 QATMDKNILKANFSVIFEELETLILLRAFTTEGAVGEISPLSPGHTNEDVKNAGV 180

DB 121 QAIMDKSILKANFSVIFDRELETLILLRAFTTEGAVGEISPLSPGHTNEDVKNAGV 180

QY 181 LIGGLKNDNTVRISSETLORFWRSSHENGSRSPPKQKMKMERTIEPEV 230

DB 181 LIGGLEWNNVTVRSKTLQRFWRSSHENGSRPPLTPKQKRMARTIRSEV 230

RESULT 12

ID ADO14180 standard; protein; 227 AA.

XX AC ADO14180;

XX DT 12-AUG-2004 (first entry)

XX DE Influenza A virus non-structural protein (NS)-1 #10.

XX KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;

XX KW double-stranded RNA; dsRNA; binding domain; virucide;

XX KW translation inhibition factor; eip2alpha; viral protein synthesis;

XX KW viral protein replication; screening method; infection.

XX OS Influenza A virus.

XX PN WO2004043404-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036292.

XX PR 13-NOV-2002; 2002US-0425661P.

XX PR 10-JUN-2003; 2003US-0477453P.

XX PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.

XX PI Montelione GT, Krug RM;

XX DR WPI: 2004-420083/39.

XX PT Identifying agents useful for treating influenza virus infection comprises identifying compounds that inhibit binding between influenza virus non-structural protein-1 (NS1) and a double-stranded RNA that binds the protein.

XX PS Disclosure; Page 13-14; 92pp; English.

XX CC This invention relates to a novel method of identifying an inhibitor of influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus non-structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding domain and a dsRNA that binds the protein. The invention may be useful for the production of compounds with a virucide activity acting as inhibitors of binding between influenza virus non-structural protein-1 (NS1) and double-stranded RNA. It is possible that binding of double-stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA-activated protein kinase to remain in an inactive state so that it does not catalyze the phosphorylation of translation inhibition factor eip2alpha, which would otherwise inhibit viral protein synthesis and replication. The invention is useful as a (high throughput) screening method for identifying compounds having inhibitory activity against

CC influenza virus. Compounds identified are useful in treating animals,  
CC including human infected with influenza virus. The present sequence is  
CC that of an influenza virus non-structural (NS)-1 protein which is related  
CC to the method of the invention.

SQ Sequence 227 AA;  
Query Match 89.2%; Score 1051; DB 8; Length 227;  
Best Local Similarity 90.3%; Pred. No. 4.1e-104; Indels 0; Gaps 0;  
Matches 205; Conservative 8; Mismatches 14; Indels 0; Gaps 0;  
QY 4 NTYSSFOVDCFLWHVYKRFADQELGADPFLDRLRRDOKSLKGRSTLGLDIETATRA 63  
DB 1 NTYSSFOVDCFLWHVYKRFADQELGADPFLDRLRRDOKSLKGRSTLGLDIETATRA 60  
QY 64 IVROITLKEESDEALKWTIASVPASRYLTDMTLDMSRDWFMMPKQVGTGSLCIRMDQAI 123  
DB 61 IVERILKEESDETLKWTIASAPAFRPTDMILEMSRDWFMMPKQVAGSLCIRMDQAI 120  
QY 124 MDKXNIIILKANFSVIFERLETLILRAFTTEGAIVGEISPLSPGHTNEDVKNAIGVLIG 183  
DB 121 MDKXNIIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHTNEDVKNAIGDLIG 180  
QY 184 GLKWNNTVRISETLQRFAMRSSHENGSRFPKPKKRMERTIEPEV 230  
DB 181 GLEWNTVRISETLQRFAMRSSNEGRRPLPPKPKKRMERTIESEV 227

RESULT 13  
AD014171  
ID AD014171 standard; protein; 230 AA.  
XX AD014171;  
DT 12-AUG-2004 (first entry)  
DE Influenza A virus non-structural protein (NS)-1 #1.  
XX Influenza inhibitor; influenza virus; non-structural protein-1; NS1;  
KW double-stranded RNA; dsRNA; binding domain; virucide;  
KW double-stranded RNA-activated protein kinase; phosphorylation;  
KW translation inhibition factor; eIF2alpha; viral protein synthesis;  
KW viral protein replication; screening method; infection.  
XX Influenza A virus; A/Udorn/307/72 (H3N2).  
OS WO2004043404-A2.  
PN 27-MAY-2004.  
XX 13-NOV-2003; 2003WO-US036292.  
XX 13-NOV-2002; 2002US-0425661P.  
PR 10-JUN-2003; 2003US-0477453P.  
XX (RUTP ) UNIV RUTGERS STATE NEW JERSEY.  
PA Montellione GT, Krug RM;  
PI WPI; 2004-420083/39.  
DR Identifying agents useful for treating influenza virus infection  
PT comprises identifying compounds that inhibit binding between influenza  
PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds  
PT the protein.  
XX Disclosure; Page 11; 92pp; English.

XX This invention relates to a novel method of identifying an inhibitor of  
XX influenza virus which comprises testing candidate compounds for their  
CC ability to reduce the extent of binding between influenza virus non-  
CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding  
CC domain and a dsRNA that binds the protein. The invention may be useful

CC for the production of compounds with a virucide activity acting as  
CC inhibitors of binding between influenza virus non-structural protein-1  
CC (NS1) and double-stranded RNA. It is possible that binding of double-  
CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA  
CC -activated protein kinase to remain in an inactive state so that it does  
CC not catalyze the phosphorylation of translation inhibition factor  
CC eIF2alpha, which would otherwise inhibit viral protein synthesis and  
CC replication. The invention is useful as a (high throughput) screening  
CC method for identifying compounds having inhibitory activity against  
CC influenza virus. Compounds identified are useful in treating animals,  
CC including human infected with influenza virus. The present sequence is  
CC that of an influenza virus non-structural (NS)-1 protein which is related  
CC to the method of the invention.

SQ Sequence 230 AA;  
Query Match 89.0%; Score 1048; DB 8; Length 230;  
Best Local Similarity 88.3%; Pred. No. 8.8e-104;  
Matches 203; Conservative 14; Mismatches 13; Indels 0; Gaps 0;  
QY 1 MDSNTVSSFOVDCFLWHVYKRFADQELGADPFLDRLRRDOKSLKGRSTLGLDIETATRA 60  
DB 1 MDPNTVSSFOVDCFLWHVYKRFADQELGADPFLDRLRRDOKSLKGRSTLGLDIETATRA 60  
QY 61 GKQIVEITLKEESDEALKWTIASVPASRYLTDMTLDMSRDWFMMPKQVGTGSLCIRMD 120  
DB 61 GKQIVERILKEESDEALKWTIASVPASRYLTDMTLDMSRDWFMMPKQVGTGSLCIRMD 120  
QY 121 QAIWMDKXNIIILKANFSVIFERLETLILRAFTTEGAIVGEISPLSPGHTNEDVKNAIGV 180  
DB 121 QAIWMDKXNIIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHTAEDVKNAIGV 180  
QY 181 LIGGLKWNNTVRISETLQRFAMRSSHENGSRFPKPKKRMERTIEPEV 230  
DB 181 LIGGLEWNTVRISETLQRFAMRSSNEGRRPLPPKPKKRMERTIESEV 230

RESULT 14  
AD014176  
ID AD014176 standard; protein; 230 AA.  
XX AD014176;  
DT 12-AUG-2004 (first entry)  
DE Influenza A virus non-structural protein (NS)-1 #6.  
XX Influenza inhibitor; influenza virus; non-structural protein-1; NS1;  
KW double-stranded RNA; dsRNA; binding domain; virucide;  
KW double-stranded RNA-activated protein kinase; phosphorylation;  
KW translation inhibition factor; eIF2alpha; viral protein synthesis;  
KW viral protein replication; screening method; infection.  
XX Influenza A virus.  
OS WO2004043404-A2.  
PN 27-MAY-2004.  
XX 13-NOV-2003; 2003WO-US036292.  
XX 13-NOV-2002; 2002US-0425661P.  
PR 10-JUN-2003; 2003US-0477453P.  
XX (RUTP ) UNIV RUTGERS STATE NEW JERSEY.  
PA Montellione GT, Krug RM;  
PI WPI; 2004-420083/39.  
DR Identifying agents useful for treating influenza virus infection  
PT comprises identifying compounds that inhibit binding between influenza  
PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds

PT the protein.  
 XX Disclosure; Page 12-13; 92pp; English.  
 XX This invention relates to a novel method of identifying an inhibitor of  
 XX influenza virus which comprises testing candidate compounds for their  
 XX ability to reduce the extent of binding between influenza virus non-  
 XX structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding  
 XX domain and a dsRNA that binds the protein. The invention may be useful  
 XX for the production of compounds with a virucide activity acting as  
 XX inhibitors of binding of compounds with influenza virus non-structural protein-1  
 XX (NS1) and double-stranded RNA. It is possible that binding of double-  
 XX stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA  
 XX activated protein kinase to remain in an inactive state so that it does  
 XX not catalyze the phosphorylation of translation inhibition factor and  
 XX eIF2alpha, which would otherwise inhibit viral protein synthesis and  
 XX replication. The invention is useful as a (high throughput) screening  
 XX method for identifying compounds having inhibitory activity against  
 XX influenza virus. Compounds identified are useful in treating animals,  
 XX including human, infected with influenza virus. The present sequence is  
 XX that of an influenza virus non-structural (NS)-1 protein which is related  
 XX to the method of the invention.

SQ Sequence 230 AA;

Query Match 88.5%; Score 1042; DB 8; Length 230;  
 Best Local Similarity 87.8%; Pred. NO. 3.9e-103;  
 Matches 202; Conservative 16; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 MDSNTVSSFQVDCFLMHWVRKRFADQELGDAPFLDLRLRDQKSLKRGSTLGLDIDETATRA 60  
 DB 1 MDSNTVSSFQVDCFLMHWVRKRFADQELGDAPFLDLRLRDQKSLKRGSTLGLDIDETATRA 60  
 QY 61 GKQIVEQILKEESDEALKMTIASVPASRYLTDMTLDEMSRDWFMMPKQKVTGSLCIRMD 120  
 DB 61 GKQIVERILEESNEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120  
 QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVGEISPLPSLPFGHTNEDVKNAGV 180  
 DB 121 QAIMKSIILKANFSVIFDRLETLILLRAFTTEGAVGEISPLPSLPFGHTNEDVKNAGV 180  
 QY 181 LIGGLKWNNDTVRISSETLQRFWRSSHENGSRPSPPKQKRWERTIEPEV 230  
 DB 181 LIGGLEWNGNTVRVSENLRFAWRSENERPSLPKQKREVACTIRSEV 230

RESULT 15

ABB05772  
 ID ABB05772 standard; protein; 237 AA.  
 XX  
 AC ABB05772;  
 XX  
 XX  
 DT 07-MAY-2002 (first entry)  
 XX  
 DE Influenza A/Udorn/72 (H3N2) Strain NS1 protein SEQ ID NO:18.  
 XX  
 KW Influenza A/Udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;  
 KW Influenza A virus; genome.  
 XX  
 OS Influenzavirus A.  
 XX  
 FN WO200200984-A2.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 21-JUN-2001; 2001WO-US019826.  
 XX  
 PR 23-JUN-2000; 2000US-0213650P.  
 XX  
 PA (AMCY ) AMERICAN CYANAMID CO.  
 XX  
 PI Galarza JM, Latham TE;  
 XX

DR WPI; 2002-139923/18.  
 XX N-PSDB; ABA93942.

PT Polynucleotide encoding complete sequence of influenza A/Udorn/72 and  
 PT polypeptide, useful in diagnosis and for generating new Influenza A  
 PT variant strains.

XX Disclosure; Page 78-79; 103pp; English.

PS The present invention describes an isolated polynucleotide (I) having the  
 CC complete sequence of the Influenza A/Udorn/72 (H3N2) strain in positive  
 CC strand, and an genomic message sense. ABA93934 to ABA93944 encode the  
 CC Influenza A/Udorn/72 (H3N2) strain proteins given in ABB05764 to ABB05774  
 CC from the present invention. (I) is useful for designing polymerase chain  
 CC reaction (PCR) primers for use in a PCR assay to detect the presence of  
 CC the corresponding virus segment in a sample or for designing and  
 CC selecting peptides for use in an enzyme linked immunosorbent assay to  
 CC detect the presence of the corresponding protein produced by that segment  
 CC in a sample, hence is useful in diagnosis and may be modified by mutation  
 CC to generate new Influenza A variant strains. ABA94945 to ABA94939  
 CC represent Influenza A/Udorn/72 (H3N2) strain sequencing primers, which  
 CC are used in an example from the present invention

XX SQ Sequence 237 AA;

Query Match 85.7%; Score 1010; DB 5; Length 237;  
 Best Local Similarity 83.9%; Pred. NO. 1.1e-99;  
 Matches 193; Conservative 19; Mismatches 18; Indels 0; Gaps 0;  
 QY 1 MDSNTVSSFQVDCFLMHWVRKRFADQELGDAPFLDLRLRDQKSLKRGSTLGLDIDETATRA 60  
 DB 1 MDSNTVSSFQVDCFLMHWVRKRVQVQELGDAPFLDLRLRDQKSLKRGSTLGLNIEAATHV 60  
 QY 61 GKQIVEQILKEESDEALKMTIASVPASRYLTDMTLDEMSRDWFMMPKQKVTGSLCIRMD 120  
 DB 61 GKQIVEKILKEESDEALKMTMASTPASRYITDMTIELSRDWFMMPKQKVEGPLCIRID 120  
 QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVGEISPLPSLPFGHTNEDVKNAGV 180  
 DB 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTTEGAVGEISPLPSFPFGHTIEDVKNAGV 180  
 QY 181 LIGGLKWNNDTVRISSETLQRFWRSSHENGSRPSPPKQKRWERTIEPEV 230  
 DB 181 LIGGLEWNGNTVRVSKTLQRFWRSSNENGSRPPLTPKQKRWARTARSKV 230

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OM protein - protein search, using sw model

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Title: US-10-734-373-58  
Perfect score: 1178  
Sequence: 1 MDSNTVSSQVDFLHVHRK.....RPSFPKQKRMERTIEPV 230

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1178	100.0	230	2 Q77ZM3_IHAH1	Q77ZM3 influenza a
2	1178	100.0	230	2 Q9VJE2_IHAH1	Q9VJE2 influenza a
3	1177	99.9	230	2 Q9VZ68_IHAH1	Q9VZ68 influenza a
4	1177	99.9	230	2 Q9VZ72_IHAH1	Q9VZ72 influenza a
5	1174	99.7	230	2 Q9VZ71_IHAH1	Q9VZ71 influenza a
6	1171	99.4	230	2 Q9VZ70_IHAH1	Q9VZ70 influenza a
7	1171	99.4	230	2 Q9VZ75_IHAH1	Q9VZ75 influenza a
8	1167	99.1	230	2 Q9VZ69_IHAH1	Q9VZ69 influenza a
9	1167	99.1	230	2 Q9VZ67_IHAH1	Q9VZ67 influenza a
10	1165	98.9	230	2 Q9VZ66_IHAH1	Q9VZ66 influenza a
11	1162	98.6	230	2 Q9VZ65_IHAH1	Q9VZ65 influenza a
12	1160	98.5	230	2 Q9VZ64_IHAH1	Q9VZ64 influenza a
13	1159	98.4	230	2 Q9VZ63_IHAH1	Q9VZ63 influenza a
14	1154	98.0	230	2 Q9VZ62_IHAH1	Q9VZ62 influenza a
15	1153	97.9	230	2 Q9VZ61_IHAH1	Q9VZ61 influenza a
16	1150	97.6	230	2 Q9VZ60_IHAH1	Q9VZ60 influenza a
17	1149	97.5	230	2 Q9VZ59_IHAH1	Q9VZ59 influenza a
18	1147	97.4	230	2 Q9VZ58_IHAH1	Q9VZ58 influenza a
19	1147	97.4	230	2 Q9VZ57_IHAH1	Q9VZ57 influenza a
20	1147	97.4	230	2 Q9VZ56_IHAH1	Q9VZ56 influenza a
21	1144	97.1	230	2 Q9VZ55_IHAH1	Q9VZ55 influenza a
22	1144	97.1	230	2 Q9VZ54_IHAH1	Q9VZ54 influenza a
23	1138	96.6	230	2 Q9VZ53_IHAH1	Q9VZ53 influenza a
24	1134	94.7	230	2 Q9VZ52_IHAH1	Q9VZ52 influenza a
25	1114	94.6	230	2 Q9VZ51_IHAH1	Q9VZ51 influenza a
26	1113	94.5	230	2 Q9VZ50_IHAH1	Q9VZ50 influenza a
27	1112	94.4	230	2 Q9VZ49_IHAH1	Q9VZ49 influenza a
28	1112	94.4	230	2 Q9VZ48_IHAH1	Q9VZ48 influenza a
29	1111	94.3	230	2 Q9VZ47_IHAH1	Q9VZ47 influenza a
30	1111	94.3	230	2 Q9VZ46_IHAH1	Q9VZ46 influenza a
31	1111	94.3	230	2 Q9VZ45_IHAH1	Q9VZ45 influenza a

32	1111	94.3	230	2 Q6DX21_9INFA	Q6DX21 influenza a
33	1111	94.3	230	2 Q6DXC5_9INFA	Q6DXC5 influenza a
34	1111	94.3	230	2 Q6DXG5_9INFA	Q6DXG5 influenza a
35	1111	94.3	230	2 Q6GYS8_9INFA	Q6GYS8 influenza a
36	1111	94.3	230	2 Q6GYS9_9INFA	Q6GYS9 influenza a
37	1111	94.3	230	2 Q6XC04_9INFA	Q6XC04 influenza a
38	1111	94.3	230	2 Q71E84_9INFA	Q71E84 influenza a
39	1111	94.3	230	2 Q71VH8_9INFA	Q71VH8 influenza a
40	1111	94.3	230	2 Q77W14_9INFA	Q77W14 influenza a
41	1111	94.3	230	2 Q7EY6_9INFA	Q7EY6 influenza a
42	1111	94.3	230	2 Q6LDH3_9INFA	Q6LDH3 influenza a
43	1110	94.2	230	2 Q7EY2_9INFA	Q7EY2 influenza a
44	1110	94.2	230	2 Q9WC09_9INFA	Q9WC09 influenza a
45	1110	94.2	230	2 Q9YPE8_9INFA	Q9YPE8 influenza a

## ALIGNMENTS

RESULT 1  
Q77ZM3\_IHAH1 PRELIMINARY; PRT; 230 AA.

AC Q77ZM3; (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Nonstructural protein NS1.  
OS Influenza A virus (strain A/Equine/Alaska/1/91 H3N8).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenzavirus A.  
OX NCBI\_TaxID=225092;  
RN [1]  
RX NUCLEOTIDE SEQUENCE.  
RP MEDLINE=98411653; PubMed=9739336; DOI=10.1007/s007050050400;  
RA Lindstrom S., Endo A., Sugita S., Pecoraio M., Hiromoto Y., Kamada M.,  
RA Takahashi T., Nerome K.;  
RT "Phylogenetic analyses of equine influenza M and NS genes and  
RT comparison with the HA gene".  
RL Arch. Virol. 143:1585-1598(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Lindstrom S.F.  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF001667; AAC31258.1; -; Genomic\_RNA.  
DR HSP; F03495; IAIL.  
DR SMR; Q77ZM3; 1-70.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR InterPro; IPR000256; Flu\_NS1.  
DR Pfam; PF00600; Flu\_NS1; 1.  
DR ProDom; PD000613; Flu\_NS1; 1.  
SQ SEQUENCE 230 AA; 26169 MW; 8CCE20B9A6CAC2E6 CRC64;

Query Match 100.0%; Score 1178; DB 2; Length 230;  
Best Local Similarity 100.0%; Pred. No. 4.8e-91;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSNTVSSQVDFLHVHRKRFADQELGDPAPFLDRLRDQKSLKGRGSLGLDIETATRA 60  
Db 1 MDSNTVSSQVDFLHVHRKRFADQELGDPAPFLDRLRDQKSLKGRGSLGLDIETATRA 60

QY 61 GKQIVQIILEESDEALKMTIASVPASRYLTDMTLDMSRDWFMPLMPKQKVTGSLCIRMD 120  
Db 61 GKQIVQIILEESDEALKMTIASVPASRYLTDMTLDMSRDWFMPLMPKQKVTGSLCIRMD 120

QY 121 QATMDKNITLKANSVIFERLETLILLRAFTEGAVGEISPLPSFGHTNEDVKNALGV 180  
Db 121 QATMDKNITLKANSVIFERLETLILLRAFTEGAVGEISPLPSFGHTNEDVKNALGV 180

QY 181 LIGLKWNDNTRISSETLQFPAWRSSHENGREPSFPKQKRMERTIEPV 230  
Db 181 LIGLKWNDNTRISSETLQFPAWRSSHENGREPSFPKQKRMERTIEPV 230

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RESULT 2
Q9YJ2 9INFA
ID Q9YJ2 9INFA PRELIMINARY; PRT; 230 AA.
AC Q9YJ2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein NS1.
OS Influenza A virus (A/eq/Kentucky/92 (H3N8)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=60025;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98411653; PubMed=9739336; DOI=10.1007/s007050050400;
RA Lindstrom S., Endo A., Sugita S., Pecoraro M., Hiromoto Y., Kanada M.,
RA Takahashi T., Nerome K.;
RT "Phylogenetic analyses of equine influenza M and NS genes and
RT comparison with the HA gene.";
RL Arch. Virol. 143:1585-1598 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lindstrom S.E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001671; AAC31266.1; -, Genomic_RNA.
DR HSSP; P03495; 1-70.
DR SMR; Q9YJ2; 1-70.
GO GO:0003723; F:RNA binding; IEA.
GO GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD000613; Flu NS1; 1.
SQ SEQUENCE 230 AA; 26155 MW; 746CAAD835D96965 CRC64;

Query Match 100.0%; Score 1178; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.8e-91;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVGVEISPLSPGHNTNEDVKNAIGV 180
DB 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVGVEISPLSPGHNTNEDVKNAIGV 180
QY 181 LIGLKWNDNTVRISETLQRFAMRSSHENGSRPSFPKQKRWERTIPEV 230
DB 181 LIGLKWNDNTVRISETLQRFAMRSSHENGSRPSFPKQKRWERTIPEV 230

RESULT 3
Q9YJ26 9INFA
ID Q9YJ26 9INFA PRELIMINARY; PRT; 230 AA.
AC Q9YJ26;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein NS1.
OS Influenza A virus (A/eq/Laplata/93 (H3N8)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=60027;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98411653; PubMed=9739336; DOI=10.1007/s007050050400;
RA Lindstrom S., Endo A., Sugita S., Pecoraro M., Hiromoto Y., Kanada M.,
RA Takahashi T., Nerome K.;
RT "Phylogenetic analyses of equine influenza M and NS genes and
RT comparison with the HA gene.";
RL Arch. Virol. 143:1585-1598 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lindstrom S.E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001666; AAC31256.1; -, Genomic_RNA.
DR HSSP; P03495; 1-70.
DR SMR; Q9YJ26; 1-70.
GO GO:0003723; F:RNA binding; IEA.
GO GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD000613; Flu NS1; 1.
SQ SEQUENCE 230 AA; 26155 MW; 8CCE20B9A6CAC2B6 CRC64;

Query Match 100.0%; Score 1178; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.8e-91;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVGVEISPLSPGHNTNEDVKNAIGV 180
DB 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVGVEISPLSPGHNTNEDVKNAIGV 180
QY 181 LIGLKWNDNTVRISETLQRFAMRSSHENGSRPSFPKQKRWERTIPEV 230
DB 181 LIGLKWNDNTVRISETLQRFAMRSSHENGSRPSFPKQKRWERTIPEV 230

RESULT 4
Q9YJ27 9INFA
ID Q9YJ27 9INFA PRELIMINARY; PRT; 230 AA.
AC Q9YJ27;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein NS1.
OS Influenza A virus (A/equine/Yvelines/2136/89 (H3N8)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=225091;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98411653; PubMed=9739336; DOI=10.1007/s007050050400;
RA Lindstrom S., Endo A., Sugita S., Pecoraro M., Hiromoto Y., Kanada M.,
RA Takahashi T., Nerome K.;
RT "Phylogenetic analyses of equine influenza M and NS genes and
RT comparison with the HA gene.";
RL Arch. Virol. 143:1585-1598 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lindstrom S.E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001666; AAC31256.1; -, Genomic_RNA.
DR HSSP; P03495; 1-70.
DR SMR; Q9YJ27; 1-70.
GO GO:0003723; F:RNA binding; IEA.
GO GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD000613; Flu NS1; 1.
SQ SEQUENCE 230 AA; 26155 MW; 8CCE20E9B572F976 CRC64;

Query Match 99.9%; Score 1177; DB 2; Length 230;
Best Local Similarity 99.6%; Pred. No. 5.8e-91;
Matches 229; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVGVEISPLSPGHNTNEDVKNAIGV 180
DB 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVGVEISPLSPGHNTNEDVKNAIGV 180
QY 181 LIGLKWNDNTVRISETLQRFAMRSSHENGSRPSFPKQKRWERTIPEV 230
DB 181 LIGLKWNDNTVRISETLQRFAMRSSHENGSRPSFPKQKRWERTIPEV 230
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Db 1 MDSNTVSSFOVDCFLMHVRRKFAADQELGADPFLDLRRDOKSLKGRGSLGLDLETATRA 60
Qy 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLTDEMSRDMFMLMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLTDEMSRDMFMLMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIIKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIIKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPPPKQKRMERTIEPEV 230
Db 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPPPKQKRMERTIEPEV 230

RESULT 5
Q9YZ71_9INFA
ID Q9YZ71_9INFA PRELIMINARY; PRT; 230 AA.
AC Q9YZ71;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Nonstructural protein NS1.
OS Influenza A virus (A/Equine/Arundel/12369/91 (H3N8)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=225093;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98411653; PubMed=9739336; DOI=10.1007/s007050050400;
RA Lindstrom S., Endo A., Sugita S., Pecoraro M., Hiromoto Y., Kamada M.,
RA Takahashi T., Nerome K.;
RT "Phylogenetic analyses of equine influenza M and NS genes and
RT comparison with the HA gene.";
RL Arch. Virol. 143:1585-1598(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98411653; PubMed=9739336; DOI=10.1007/s007050050400;
RA Lindstrom S., Endo A., Sugita S., Pecoraro M., Hiromoto Y., Kamada M.,
RA Takahashi T., Nerome K.;
RT "Phylogenetic analyses of equine influenza M and NS genes and
RT comparison with the HA gene.";
RL Arch. Virol. 143:1585-1598(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lindstrom S.E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001669; AAC31260.1; -; Genomic_RNA.
DR HSSP; P03495; NS1.
DR SMR; Q9YZ71; 1-70.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD000613; Flu NS1; 1.
SQ SEQUENCE 230 AA; 26183 MW; 8DBB20E9A78FC213 CRC64;

Query Match 99.7%; Score 1174; DB 2; Length 230;
Best Local Similarity 99.6%; Pred. No. 1e-90;
Matches 229; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLMHVRRKFAADQELGADPFLDLRRDOKSLKGRGSLGLDLETATRA 60
Db 1 MDSNTVSSFOVDCFLMHVRRKFAADQELGADPFLDLRRDOKSLKGRGSLGLDLETATRA 60
Qy 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLTDEMSRDMFMLMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLTDEMSRDMFMLMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIIKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIIKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPPPKQKRMERTIEPEV 230
Db 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPPPKQKRMERTIEPEV 230

RESULT 6
Q9YZ70_9INFA
ID Q9YZ70_9INFA PRELIMINARY; PRT; 230 AA.
```

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AC Q9YZ70;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Nonstructural protein NS1.
OS Influenza A virus (A/eq/Roma/5/91 (H3N8)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=60023;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98411653; PubMed=9739336; DOI=10.1007/s007050050400;
RA Lindstrom S., Endo A., Sugita S., Pecoraro M., Hiromoto Y., Kamada M.,
RA Takahashi T., Nerome K.;
RT "Phylogenetic analyses of equine influenza M and NS genes and
RT comparison with the HA gene.";
RL Arch. Virol. 143:1585-1598(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lindstrom S.E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001669; AAC31262.1; -; Genomic_RNA.
DR HSSP; P03495; NS1.
DR SMR; Q9YZ70; 1-70.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD000613; Flu NS1; 1.
SQ SEQUENCE 230 AA; 26201 MW; 144DE000EB6851C0 CRC64;

Query Match 99.4%; Score 1171; DB 2; Length 230;
Best Local Similarity 98.7%; Pred. No. 1.9e-90;
Matches 227; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLMHVRRKFAADQELGADPFLDLRRDOKSLKGRGSLGLDLETATRA 60
Db 1 MDSNTVSSFOVDCFLMHVRRKFAADQELGADPFLDLRRDOKSLKGRGSLGLDLETATRA 60
Qy 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLTDEMSRDMFMLMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLTDEMSRDMFMLMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIIKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIIKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPPPKQKRMERTIEPEV 230
Db 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPPPKQKRMERTIEPEV 230

RESULT 7
Q9YZ75_9INFA
ID Q9YZ75_9INFA PRELIMINARY; PRT; 230 AA.
AC Q9YZ75;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Nonstructural protein NS1.
OS Influenza A virus (A/eq/Kentucky/1/88 (H3N8)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=60030;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98411653; PubMed=9739336; DOI=10.1007/s007050050400;
RA Lindstrom S., Endo A., Sugita S., Pecoraro M., Hiromoto Y., Kamada M.,
RA Takahashi T., Nerome K.;
RT "Phylogenetic analyses of equine influenza M and NS genes and
RT comparison with the HA gene.";
RL Arch. Virol. 143:1585-1598(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
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Wed Mar 8 09:11:20 2006

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RA Lindstrom S.E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001664; AAC31252.1; -, Genomic_RNA.
DR HSP; P03495; INS1.
DR SMR; Q9Y269; 1-70.
DR GO; GO:0003723; P: RNA binding; IEA.
DR InterPro; IPR000256; Flu_NS1.
DR Pfam; PF00600; Flu_NS1; 1.
DR ProDom; PD000613; Flu_NS1; 1.
SQ SEQUENCE 230 AA; 26097 MW; 38CE20E9B572F970 CRC64;

Query Match 99.4%; Score 1171; DB 2; Length 230;
Best Local Similarity 99.1%; Pred. No. 1; 9e-90;
Matches 228; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDSNTVSSQVDCFLMHVRRKRFADQELGDAPFLDRDQKSLKRGSTGLDLETATRA 60
DB 1 MDSNTVSSQVDCFLMHVRRKRFADQELGDAPFLDRDQKSLKRGSTGLDLETATRA 60

QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120

QY 121 QAIMDKNIILKANFSVIFERLETILLRAFTTEGAVVGEISPLSPKPGHNTNEDVKNAGV 180
DB 121 QAIMDKNIILKANFSVIFERLETILLRAFTTEGAVVGEISPLSPKPGHNTNEDVKNAGV 180

QY 181 LIGLKWNDNTVRISSETLQRFAMRSSHENGSRPFPKQKRMERTIEPEV 230
DB 181 LIGLKWNDNTVRISSETLQRFAMRSSHENGSRPFPKQKRMERTIEPEV 230

Query Match 99.1%; Score 1167; DB 2; Length 230;
Best Local Similarity 98.7%; Pred. No. 4e-90;
Matches 227; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSNTVSSQVDCFLMHVRRKRFADQELGDAPFLDRDQKSLKRGSTGLDLETATRA 60
DB 1 MDSNTVSSQVDCFLMHVRRKRFADQELGDAPFLDRDQKSLKRGSTGLDLETATRA 60

QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120

QY 121 QAIMDKNIILKANFSVIFERLETILLRAFTTEGAVVGEISPLSPKPGHNTNEDVKNAGV 180
DB 121 QAIMDKNIILKANFSVIFERLETILLRAFTTEGAVVGEISPLSPKPGHNTNEDVKNAGV 180

QY 181 LIGLKWNDNTVRISSETLQRFAMRSSHENGSRPFPKQKRMERTIEPEV 230
DB 181 LIGLKWNDNTVRISSETLQRFAMRSSHENGSRPFPKQKRMERTIEPEV 230

Query Match 99.1%; Score 1167; DB 2; Length 230;
Best Local Similarity 98.7%; Pred. No. 4e-90;
Matches 227; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSNTVSSQVDCFLMHVRRKRFADQELGDAPFLDRDQKSLKRGSTGLDLETATRA 60
DB 1 MDSNTVSSQVDCFLMHVRRKRFADQELGDAPFLDRDQKSLKRGSTGLDLETATRA 60
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QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120

QY 121 QAIMDKNIILKANFSVIFERLETILLRAFTTEGAVVGEISPLSPKPGHNTNEDVKNAGV 180
DB 121 QAIMDKNIILKANFSVIFERLETILLRAFTTEGAVVGEISPLSPKPGHNTNEDVKNAGV 180

QY 181 LIGLKWNDNTVRISSETLQRFAMRSSHENGSRPFPKQKRMERTIEPEV 230
DB 181 LIGLKWNDNTVRISSETLQRFAMRSSHENGSRPFPKQKRMERTIEPEV 230

RESULT 9
QYVZ69 9INFA PRELIMINARY; PRT; 230 AA.
AC QYVZ69;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein NS1.
OS Influenza A virus (A/Hong Kong/1/92 (H3N8)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OC NCBI_TaxID=60024;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98411653; PubMed=9739336; DOI=10.1007/s007050050400;
RA Lindstrom S.; Endo A.; Sugita S.; Pecoraro M.; Hiromoto Y.; Kamada M.;
RA Takahashi T.; Nerome K.;
RA "Phylogenetic analyses of equine influenza M and NS genes and
RT comparison with the HA gene."
RL Arch. Virol. 143:1585-1598 (1998).
[2]
RN NUCLEOTIDE SEQUENCE.
RX Lindstrom S.E.; 1997) to the EMBL/GenBank/DBJ databases.
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001670; AAC31264.1; -, Genomic_RNA.
DR HSP; P03495; INS1.
DR SMR; Q9Y269; 1-70.
DR GO; GO:0003723; P: RNA binding; IEA.
DR InterPro; IPR000256; Flu_NS1.
DR Pfam; PF00600; Flu_NS1; 1.
DR ProDom; PD000613; Flu_NS1; 1.
DR ProDom; PD000613; Flu_NS1; 1.
SQ SEQUENCE 230 AA; 26195 MW; 88080F5EF872E853 CRC64;

Query Match 99.1%; Score 1167; DB 2; Length 230;
Best Local Similarity 98.7%; Pred. No. 4e-90;
Matches 227; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSNTVSSQVDCFLMHVRRKRFADQELGDAPFLDRDQKSLKRGSTGLDLETATRA 60
DB 1 MDSNTVSSQVDCFLMHVRRKRFADQELGDAPFLDRDQKSLKRGSTGLDLETATRA 60

QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120

QY 121 QAIMDKNIILKANFSVIFERLETILLRAFTTEGAVVGEISPLSPKPGHNTNEDVKNAGV 180
DB 121 QAIMDKNIILKANFSVIFERLETILLRAFTTEGAVVGEISPLSPKPGHNTNEDVKNAGV 180

QY 181 LIGLKWNDNTVRISSETLQRFAMRSSHENGSRPFPKQKRMERTIEPEV 230
DB 181 LIGLKWNDNTVRISSETLQRFAMRSSHENGSRPFPKQKRMERTIEPEV 230

RESULT 10
QYVZ69 9INFA PRELIMINARY; PRT; 230 AA.
AC QYVZ69;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
```

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 GN Name=NSI;  
 OS Influenza A virus (A/equine 2/Suffolk/89 (H3N8)).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A  
 OX NCBI\_TaxID=207256;  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=Suffolk/89;  
 RX MEDLINE=97330490; PubMed=9186949; DOI=10.1016/S0168-0934(97)02189-7;  
 RA Birch-Machin I., Rowan A., Pick J., Mumford J., Binns M.;  
 RT Expression of the nonstructural protein NSI of equine influenza A  
 virus: detection of anti-NSI antibody in post infection equine sera.";  
 RL J. Virol. Methods 65:255-263 (1997).  
 DR EMBL; X80060; CAA56366.1; -; Genomic\_RNA.  
 DR HSP; P03495; INS1.  
 DR SMR; Q8JKE7; 1-70.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR InterPro; IPR000256; Flu\_NSI.  
 DR Pfam; PF00600; Flu\_NSI; 1.  
 DR ProDom; PD000613; Flu\_NSI; 1.  
 SQ SEQUENCE 230 AA; 26179 MW; 622A6C79F5D8F97C CRC64;

Query Match 98.9%; Score 1165; DB 2; Length 230;  
 Best Local Similarity 98.7%; Pred. No. 6e-90;  
 Matches 227; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MDSNTVSSFOVDCFLWHVRRKPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60  
 DB 1 MDSNTVSSFOVDCFLWHVRRKPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60  
 QY 61 GKQIVEQLLEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120  
 DB 61 GKQIVEQLLEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120  
 QY 121 QAIMDKNIIILKANFSVIFERLETLILRAFTEGAVGVEISPLPSLPGHTNEDVKNAGV 180  
 DB 121 QAIMDKNIIILKANFSVIFERLETLILRAFTEGAVGVEISPLPSLPGHTNEDVKNAGV 180  
 QY 181 LIGLKWNDNTVRISSETLQRFARSSHENGRSPFPKQKRMERTIEPV 230  
 DB 181 LIGLKWNDNTVRISSETLQRFARSSHENGRSPFPKQKRMERTIEPV 230

RESULT 11  
 Q9WA92\_9INFA  
 ID Q9WA92\_9INFA PRELIMINARY; PRT; 230 AA.  
 AC Q9WA92;  
 DT 01-NOV-1999 (TReMBLrel. 12, Created)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
 DE Nonstructural protein.  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A.  
 OX NCBI\_TaxID=11320;  
 RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=98391506; PubMed=9725667; DOI=10.1016/S0168-1702(98)00038-0;  
 RA Kawoka Y., Gorman O.T., Ito T., Wells K., Donis R.O., Castrucci M.R.,  
 RA Donatelli I., Webster R.G.;  
 RT "Influence of host species on the evolution of the nonstructural (NS)  
 gene of influenza A viruses";  
 RL Virus Res. 55:143-156 (1998).  
 DR EMBL; M80973; AAC35583.1; -; Unassigned\_RNA.  
 DR HSP; P03495; INS1.  
 DR SMR; Q9WA92; 1-70.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR InterPro; IPR000256; Flu\_NSI.  
 DR Pfam; PF00600; Flu\_NSI; 1.  
 DR ProDom; PD000613; Flu\_NSI; 1.  
 SQ SEQUENCE 230 AA; 26078 MW; C2C99E97B0A144DD CRC64;

Query Match 98.6%; Score 1162; DB 2; Length 230;  
 Best Local Similarity 98.3%; Pred. No. 1.1e-89;  
 Matches 226; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MDSNTVSSFOVDCFLWHVRRKPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60  
 DB 1 MDSNTVSSFOVDCFLWHVRRKPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60  
 QY 61 GKQIVEQLLEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120  
 DB 61 GKQIVEQLLEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120  
 QY 121 QAIMDKNIIILKANFSVIFERLETLILRAFTEGAVGVEISPLPSLPGHTNEDVKNAGV 180  
 DB 121 QAIMDKNIIILKANFSVIFERLETLILRAFTEGAVGVEISPLPSLPGHTNEDVKNAGV 180  
 QY 181 LIGLKWNDNTVRISSETLQRFARSSHENGRSPFPKQKRMERTIEPV 230  
 DB 181 LIGLKWNDNTVRISSETLQRFARSSHENGRSPFPKQKRMERTIEPV 230

RESULT 12  
 Q9YPE0\_9INFA  
 ID Q9YPE0\_9INFA PRELIMINARY; PRT; 230 AA.  
 AC Q9YPE0;  
 DT 01-MAY-1999 (TReMBLrel. 10, Created)  
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
 DE Nonstructural protein.  
 OS Influenza A virus.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A.  
 OX NCBI\_TaxID=11320;  
 RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=98391506; PubMed=9725667; DOI=10.1016/S0168-1702(98)00038-0;  
 RA Kawoka Y., Gorman O.T., Ito T., Wells K., Donis R.O., Castrucci M.R.,  
 RA Donatelli I., Webster R.G.;  
 RT "Influence of host species on the evolution of the nonstructural (NS)  
 gene of influenza A viruses";  
 RL Virus Res. 55:143-156 (1998).  
 DR EMBL; M80971; AAC35581.1; -; Unassigned\_RNA.  
 DR HSP; P03495; INS1.  
 DR SMR; Q9YPE0; 1-70.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR InterPro; IPR000256; Flu\_NSI.  
 DR Pfam; PF00600; Flu\_NSI; 1.  
 DR ProDom; PD000613; Flu\_NSI; 1.  
 SQ SEQUENCE 230 AA; 26129 MW; 97CDD1F79728D0CF CRC64;

Query Match 98.5%; Score 1160; DB 2; Length 230;  
 Best Local Similarity 98.7%; Pred. No. 1.6e-89;  
 Matches 227; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MDSNTVSSFOVDCFLWHVRRKPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60  
 DB 1 MDSNTVSSFOVDCFLWHVRRKPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60  
 QY 61 GKQIVEQLLEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120  
 DB 61 GKQIVEQLLEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120  
 QY 121 QAIMDKNIIILKANFSVIFERLETLILRAFTEGAVGVEISPLPSLPGHTNEDVKNAGV 180  
 DB 121 QAIMDKNIIILKANFSVIFERLETLILRAFTEGAVGVEISPLPSLPGHTNEDVKNAGV 180  
 QY 181 LIGLKWNDNTVRISSETLQRFARSSHENGRSPFPKQKRMERTIEPV 230  
 DB 181 LIGLKWNDNTVRISSETLQRFARSSHENGRSPFPKQKRMERTIEPV 230

RESULT 13

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Q9W9X6_9INFA
ID Q9W9X6_9INFA PRELIMINARY; PRT; 230 AA.
AC Q9W9X6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Nonstructural protein.
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=11320;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98391506; PubMed=9725667; DOI=10.1016/S0168-1702(98)00038-0;
RA Kawaka Y., Gorman O.T., Ito T., Wells K., Donis R.O., Castrucci M.R.,
RA Donatelli I., Webster R.G.;
RT "Influence of host species on the evolution of the nonstructural (NS)
RT gene of influenza A viruses.";
RL Virus Res. 55:143-156(1998).
DR EMBL; M80976; AAC35584.1; -; Unassigned_RNA.
DR EMBL; M80954; AAC35572.1; -; Unassigned_RNA.
DR HSSP; P03495; 1NS1.
DR SMR; Q9W9X6; 1-70.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD00613; Flu NS1; 1.
DR SEQUENCE 230 AA; 26115 MW; 97CDD1E78490EB5F CRC64;

Query Match 98.4%; Score 1159; DB 2; Length 230;
Best Local Similarity 98.3%; Pred. No. 1.9e-89;
Matches 226; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLWHVVKRFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Db 1 MDSNTVSSFOVDCFLWHVVKRFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Qy 61 GKQIVEOILLESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVERILLESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGVEISPLPSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGVEISPLPSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNTVRISETLQRFAPWRSSSHENGSRPSPFPKQKRMARTIESEV 230
Db 181 LIGGLKWNNTVRISETLQRFAPWRSSSHENGSRPSPFPKQKRMARTIESEV 230
Qy SEQUENCE 230 AA; 26115 MW; 97CDD1E78490EB5F CRC64;

Query Match 98.4%; Score 1159; DB 2; Length 230;
Best Local Similarity 98.3%; Pred. No. 1.9e-89;
Matches 226; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLWHVVKRFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Db 1 MDSNTVSSFOVDCFLWHVVKRFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Qy 61 GKQIVEOILLESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVERILLESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGVEISPLPSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGVEISPLPSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNTVRISETLQRFAPWRSSSHENGSRPSPFPKQKRMARTIESEV 230
Db 181 LIGGLKWNNTVRISETLQRFAPWRSSSHENGSRPSPFPKQKRMARTIESEV 230
Qy SEQUENCE 230 AA; 26115 MW; 97CDD1E78490EB5F CRC64;

Query Match 98.4%; Score 1159; DB 2; Length 230;
Best Local Similarity 98.3%; Pred. No. 1.9e-89;
Matches 226; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLWHVVKRFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Db 1 MDSNTVSSFOVDCFLWHVVKRFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Qy 61 GKQIVEOILLESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVERILLESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGVEISPLPSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGVEISPLPSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNTVRISETLQRFAPWRSSSHENGSRPSPFPKQKRMARTIESEV 230
Db 181 LIGGLKWNNTVRISETLQRFAPWRSSSHENGSRPSPFPKQKRMARTIESEV 230
Qy SEQUENCE 230 AA; 26115 MW; 97CDD1E78490EB5F CRC64;

Query Match 98.4%; Score 1159; DB 2; Length 230;
Best Local Similarity 98.3%; Pred. No. 1.9e-89;
Matches 226; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLWHVVKRFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Db 1 MDSNTVSSFOVDCFLWHVVKRFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Qy 61 GKQIVEOILLESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVERILLESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGVEISPLPSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGVEISPLPSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNTVRISETLQRFAPWRSSSHENGSRPSPFPKQKRMARTIESEV 230
Db 181 LIGGLKWNNTVRISETLQRFAPWRSSSHENGSRPSPFPKQKRMARTIESEV 230
Qy SEQUENCE 230 AA; 26115 MW; 97CDD1E78490EB5F CRC64;
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DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD00613; Flu NS1; 1.
SQ SEQUENCE 230 AA; 26143 MW; C1CDD7F501F12932 CRC64;

Query Match 98.0%; Score 1154; DB 2; Length 230;
Best Local Similarity 98.3%; Pred. No. 5e-89;
Matches 226; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLWHVVKRFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Db 1 MDSNTVSSFOVDCFLWHVVKRFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Qy 61 GKQIVEOILLESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVERILLESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGVEISPLPSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGVEISPLPSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNTVRISETLQRFAPWRSSSHENGSRPSPFPKQKRMARTIESEV 230
Db 181 LIGGLKWNNTVRISETLQRFAPWRSSSHENGSRPSPFPKQKRMARTIESEV 230
Qy SEQUENCE 230 AA; 26143 MW; 7723D1178E3AE1FF CRC64;

Query Match 97.9%; Score 1153; DB 2; Length 230;
Best Local Similarity 97.8%; Pred. No. 6.1e-89;
Matches 225; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLWHVVKRFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Db 1 MDSNTVSSFOVDCFLWHVVKRFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Qy 61 GKQIVEOILLESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVERILLESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGVEISPLPSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGVEISPLPSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNTVRISETLQRFAPWRSSSHENGSRPSPFPKQKRMARTIESEV 230
Db 181 LIGGLKWNNTVRISETLQRFAPWRSSSHENGSRPSPFPKQKRMARTIESEV 230
Qy SEQUENCE 230 AA; 26081 MW; 7723D1178E3AE1FF CRC64;

Query Match 97.9%; Score 1153; DB 2; Length 230;
Best Local Similarity 97.8%; Pred. No. 6.1e-89;
Matches 225; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLWHVVKRFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Db 1 MDSNTVSSFOVDCFLWHVVKRFPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Qy 61 GKQIVEOILLESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVERILLESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGVEISPLPSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGVEISPLPSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNTVRISETLQRFAPWRSSSHENGSRPSPFPKQKRMARTIESEV 230
Db 181 LIGGLKWNNTVRISETLQRFAPWRSSSHENGSRPSPFPKQKRMARTIESEV 230
Qy SEQUENCE 230 AA; 26081 MW; 7723D1178E3AE1FF CRC64;
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Db 181 LIGGLKWDNTVRVSETLQRFARSSHENGSRFPFPKQKRMARTIESEV 230

Search completed: March 7, 2006, 19:21:03  
Job time : 233 secs

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